

Gencore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 2, 2004, 12:27:40 ; Search time 68 Seconds
(without alignments)
33.942 Million cell updates/sec

Title: US-10-036-492-6
Perfect score: 121
Sequence: 1 VNLQLLARYLNSQASAYYILK 24

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : PIR 76.1*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query	Match	Length	DB ID	Description
1	59	48.8	824	2	I52835	H-NUC - human
2	53	43.8	777	2	G90666	C;Species: Homo sapiens (man)
3	53	43.8	796	2	B85517	C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 01-Dec-2000
4	48	39.7	501	2	T16084	C;Accession: 152835; S53647; I37726
5	47	38.8	298	2	C97183	R;Chen, P.I.; Deng, Y.C.; Dufree, T.; Chen, K.C.; Yang-Feng, T.; Lee, W.H.
6	46	38.0	173	2	C71066	Cell Growth Differ. 6, 199-210, 1995
7	46	38.0	300	2	B56118	A;Title: Identification of a human homologue of yeast nuc2 which interacts with the ret
8	46	38.0	437	2	T47831	A;Reference number: I52835; PMID:35275339; PMID:1756179
9	46	38.0	520	2	A56118	A;Accession: 152835
10	46	38.0	806	2	A53256	A;Molecule type: mRNA
11	46	38.0	1332	2	T15670	A;Residues: 1-824 <RES>
12	45	37.2	161	2	F64038	A;Cross-references: GB:S78234; PID:998471; PID:NAAB34378_1; PID:9998472
13	45	37.2	455	2	S66765	R;Tugendreich, S.; Boguski, M.S.; Seldin, M.S.; Hietter, P.
14	45	37.2	1459	2	T24088	Proc. Natl. Acad. Sci. U.S.A. 90, 1031-1035, 1993
15	44.5	36.8	631	2	S39835	A;Title: Linking yeast genetics to mammalian genomes: identification and mapping of the
16	44	36.4	222	2	G82361	A;Reference number: A48792; PMID:8234252
17	44	36.4	504	2	S44783	A;Accession: S53646
18	43.5	36.0	53	2	S72388	A;Status: nucleic acid sequence not shown
19	43.5	36.0	173	2	C71484	A;Molecule type: mRNA
20	43.5	36.0	1102	2	T39943	A;Residues: 1-118 <TUW>
21	43	36.0	1390	2	T14004	A;Cross-references: EMBL:U00001; NID:9405832; PID:9405833
22	43	35.5	266	2	G89797	A;Gene: GDB:CDG27; DOS
23	43	35.5	325	1	XYECPA	A;Cross-references: GDB:291218; OMIM:116946
24	43	35.5	413	2	AC2360	A;Map position: 17pter-17qter
25	43	35.5	423	2	F86313	C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat homology <TT1> P499-532/Domain: tetratricopeptide repeat homology <TT1>
26	43	35.5	440	2	JS0374	F;533-567/Domain: tetratricopeptide repeat homology <TT2> P;567-600/Domain: tetratricopeptide repeat homology <TT3> P;601-634/Domain: tetratricopeptide repeat homology <TT4> F;635-668/Domain: tetratricopeptide repeat homology <TT5> F;669-702/Domain: tetratricopeptide repeat homology <TT6> F;703-736/Domain: tetratricopeptide repeat homology <TT7> F;737-770/Domain: tetratricopeptide repeat homology <TT8>
27	43	35.5	558	2	C42526	Query Match Score 59; DB 2; Length 824;
28	43	35.5	558	2	JQ1798	Best Local Similarity 54.5%; Pred. No. 0.4;
29	43	35.5	889	2	T45691	Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 LOIARCYLSASQASAYYILK 24
Db 41 LPLATCYRSRGKAYRILK 62

RESULT 2
 Probable DNA primase [Imported] - Escherichia coli (strain O157:H7, substrate RIMD 05099
 C;Species: Escherichia coli
 C;Accession: G90666
 R/Hayashi, T.; Makino, K.; Ueda, Y.; Makino, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A;Reference number: A99629; MUID:21156231; PMID:11287956
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-777 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BAE33726.1; PID:913359760; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrate RIMD 0509952
 C;Genetics:
 A;Gene: EC50303
 C;Superfamily: phage P4 DNA primase
 Query Match 43.8% Score 53; DB 2; Length 777;
 Best Local Similarity 35.7%; Pred. No. 3.3;
 Matches 10; Conservative 8; Mismatches 6; Indels 4; Gaps 1;
 Qy 1 VNQLL---ARCYLSNSQAYSAYIILK 24
 Db 174 VNQLINANGGKCFLKGGQVKNAYFYLVE 201

RESULT 3
 B85517 alpha replication protein of prophage CP-9331 [Imported] - Escherichia coli (strain O157
 C;Species: Escherichia coli
 C;Accession: B85517
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: B85517
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-796 <STO>
 A;Cross-references: GB:AE005174; PIDN:912513053; PID:912513053; GSPDB:GN00145; UWGP:203
 C;Genetics:
 A;Gene: 20339
 C;Superfamily: phage P4 DNA primase
 Query Match 43.8% Score 53; DB 2; Length 796;
 Best Local Similarity 35.7%; Pred. No. 3.4;
 Matches 10; Conservative 8; Mismatches 6; Indels 4; Gaps 1;
 Qy 1 VNQLL---ARCYLSNSQAYSAYIILK 24
 Db 193 VNQLINANGGKCFLKGGQVKNAYFYLVE 220

RESULT 4
 T16084 hypothetical protein F16H11.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T16084
 R/Wu, X.
 A;Description: The sequence of C. elegans cosmid F16H11.
 A;Accession: T16084

A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-501 <WIK>
 A;Cross-references: EMBL:U55376; NID:91280130; PIDN:g1280130; GSPDB:GN001
 C;Genetics:
 A;Gene: CESP-F16H11.1
 A;Map Position: X
 A;Introns: 18/3; 41/1; 81/3; 117/1; 163/3; 187/2; 224/3; 255/2; 283/3; 314/3; 346/3; 40:
 Query Match 39.7% Score 48; DB 2; Length 501;
 Best Local Similarity 45.0%; Pred. No. 13;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Qy 3 IQLIACYLSNSQAYSAYI 22
 Db 287 LYNNRXYINTNSQVFPFYI 306

RESULT 5
 C97183 probable nucleotidyltransferase [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum ATCC824
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C;Accession: C97183
 R/Rolling, J.; Bratton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
 J.; Daly, M.J.; Bennett, G.N.; Kooinin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4822-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: C97183
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-298 <KUR>
 A;Cross-references: GB:AE001437; PIDN:AAK80254.1; PID:915025303; GSPDB:GN00168
 C;Genetics:
 A;Gene: CAC2298
 Query Match 38.8% Score 47; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 IARCYLSNSQAYSAYI 21
 Db 142 LCKXLYNNRKYIPTAY 157

RESULT 6
 C71066 hypothetical protein PH1225 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
 C;Accession: C71066
 R/Kawarabayasi, Y.; Savada, M.; Horikawa, H.; Haikawa, Y.; Hano, S.; Seki, M.; Ohfuki, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A;Reference number: A71000; MUID:9834437; PMID:9679194
 A;Accession: C71066
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-173 <KAW>
 A;Cross-references: GB:AP000005; NID:93236132; PIDN:BAA30325.1; PID:d1031268; PID:93257:
 A;Experimental source: strain OR3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1225
 Query Match 38.0% Score 46; DB 2; Length 173;
 Best Local Similarity 45.8%; Pred. No. 9.6;
 Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 VNQLIARCYLSNSQAYSAYTILK 24
 Db : : | : | : | : | : |
 62 VGIVLWAIICYFQVSKAYKAGKLUK 85

RESULT 7
 B56118 vетиспирадиен synthase 2 - Hyoscyamus muticus (fragment)
 C:Species: Hyoscyamus muticus
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 29-Sep-1999

A:Title: Cloning and bacterial expression of a sesquiterpene cyclase from *Hyoscyamus muticus*
 A:Reference number: A56118; MUID:95221394; PMID:7706281
 A:Accession: B56118
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Accession: 1300 <BAC>
 A:Cross-references: GB:U20188; PIDN:AAA86338.1; PID:9763425
 C:Superfamily: vетиспирадиен synthase 1

Query Match 38.0%; Score 46; DB 2; Length 520;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 YLSNSQAYSAYTIL 23
 Db 366 YLSNALATSTYLL 379

RESULT 10
 A53256 nuclear protein bimA - *Emericella nidulans*
 C:Species: *Emericella nidulans*, *Aspergillus nidulans*
 C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 21-Jul-2000
 C:Accession: A53256; S21860
 R:O'Donnell, K.L.; Osman, A.H.; Morris, N.R.
 J. Cell Sci. 99, 711-719, 1991
 A:Title: bimA encodes a member of the tetratricopeptide repeat family of proteins and
 A:Reference number: A53256; MUID:92121243; PMID:177001
 A:Accession: A53256
 A:Molecule type: mRNA
 A:Residues: 1-806 <OAD>
 A:Cross-references: EMBL:X593269; PID:923334; PMID:CAA41959.1; PID:976335
 C:Genetics:
 A:Gene: bimA
 C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
 C:Keywords: mitosis; nucleus; tandem repeat homology <TT1>
 F:513-546/Domain: tetratricopeptide repeat homology <TT1>
 F:547-580/Domain: tetratricopeptide repeat homology <TT2>
 F:581-614/Domain: tetratricopeptide repeat homology <TT3>
 F:611-648/Domain: tetratricopeptide repeat homology <TT4>
 F:649-682/Domain: tetratricopeptide repeat homology <TT5>
 F:683-716/Domain: tetratricopeptide repeat homology <TT6>
 F:717-750/Domain: tetratricopeptide repeat homology <TT7>
 F:751-784/Domain: tetratricopeptide repeat homology <TT8>
 Query Match 38.0%; Score 46; DB 2; Length 806;
 Best Local Similarity 56.2%; Pred. No. 42;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 LLARCYLSNSQAYSAY 20
 Db 48 LLARYLTLONGQVZKAW 63

RESULT 11
 T15670 hypothetical protein C27H5.15 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15670
 R:Pauley, A.
 A:Description: The sequence of *C. elegans* cosmid C27H5.
 A:Reference number: Z18386
 A:Accession: T15670
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1332 <PAU>
 A:Cross-references: EMBL:U14635; PID:9540265; PID:9540271; PIDN:AAC46659.1; CESP:C27H5
 C:Genetics:
 A:Gene: CESP:C27H5.5
 A:Introns: 27/2; 93/3; 203/1; 336/1; 358/2; 394/3; 473/2; 489/3; 531/3; 574/2; 636/3;

Query Match 38.0%; Score 46; DB 2; Length 1332;
 Best Local Similarity 50.0%; Pred. No. 68;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 9
 A56118 ветиспирадиен synthase 1 - Hyoscyamus muticus (fragment)
 C:Species: Hyoscyamus muticus
 C:Accession: A56118
 R:Back, K.; Chappell, J.
 J. Biol. Chem. 270, 7375-7381, 1995
 A:Title: Cloning and bacterial expression of a sesquiterpene cyclase from *Hyoscyamus muticus*
 A:Reference number: A56118; MUID:95221394; PMID:7706281
 A:Accession: A56118
 A:Status: preliminary
 A:Molecule type: mRNA

Qy 5 LLARCYLSNSQAYSAY 20
 Db :|||: :||: :||:
 936 MLARCYVRNKKPQSAW 951

RESULT 12
 F64038 hypothetical protein HI1622 - Haemophilus influenzae (strain Rd KW20)
 C;Species: Haemophilus influenzae
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
 C;Accession: F64038
 C;Cross-references: GB:U32835; GB:L42023; NID:91574471; PID:91574471;
 C;Superfamily: Haemophilus influenzae hypothetical protein HI1622

Query Match	Score 45;	DB 2;	Length 161;
Best Local Similarity	50.2%;	Pred. No. 13;	
Matches	3;	Mismatches	0;
Qy	5 LLARCYLSNSQAYSAY 20	Db	10 LFAACTLPNAYAHLY 25

A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues 1-161 <TRIGR>
 A;Cross-references: EMBL:Z70287; PIDN:CAA94300.1; GSPDB:GN00022; CESP:RO9E10.5
 A;Experimental source: Clone RO9E10
 C;Genetics:

A;Gene: CESP:RO9E10.5
 A;Map Position: 4
 A;Intron: 86/1; 128/3; 392/1; 504/3; 723/3; 763/2; 819/3; 865/1; 1108/1; 1168/2; 1197/
 Query Match 37.2%; Score 45; DB 2; Length 1459;
 Best Local Similarity 58.3%; Pred. No. 1.1e-02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 9 CYLMSGAYSAY 20
 Db 739 CYMSNNIYSSY 750

RESULT 13
 S39835 hypothetical protein YBL052c - yeast (Saccharomyces cerevisiae)
 N;Alternative names: hypothetical protein YBL052c; hypothetical protein YBL0515
 C;Species: Saccharomyces cerevisiae
 C;Date: 16-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 29-Oct-1999
 C;Accession: S39835; S45787; S7336
 R.Scherens, B.; el Bakkoury, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.
 Yeast 9, 135-1371, 1993
 A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of Y
 A;Reference number: S39824; PMID:94205266; PMID:8154187
 A;Accession: S39835
 A;Molecule type: DNA
 A;Residues: 1-831 <SCR>
 A;Cross-references: ENBL:223261; NID:933733; PIDN:CAA0794.1; PID:9313745
 A;Experimental source: strain S288C
 R.Dubois, E.; el Bakkoury, M.; Glandsorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.
 submitted to the Protein Sequence Database, August 1994
 A;Reference number: S45782
 A;Accession: S45787
 A;Molecule type: DNA
 A;Residues: 1-831 <DUB>
 A;Cross-references: ENBL:235814; NID:9536078; PIDN:CAA84873.1; PID:9536080; MIPS:YBL05:
 A;Experimental source: strain S288C
 C;Genetics:

A;Gene: SGD:SAS3
 A;Cross-references: SGD:S0000148; MIPS:YBL052C
 A;Map Position: 2L

Query Match 36.8%; Score 44.5; DB 2; Length 831;
 Best Local Similarity 37.0%; Pred. No. 74;
 Matches 10; Conservative 6; Mismatches 6; Indels 5; Gaps 1;

Qy	2 NLQLARCYLSNSQAY----SAYIL 23	Db	355 NLCLAKCPINSKTLYYDVEPPFFYIL 381
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Search completed: February 2, 2004, 13:02:38
 Job time : 69 secs

RESULT 14
 T21088 hypothetical protein RO9E10.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T24088
 R.Matthews, L.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z19839

Qy 5 LLARCYLSNSQAYSAY 20
 Db 225 LLGRYYLLNSQVNNAF 240

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DR: U00001; AAB60471.1; -

DR: S78234; AAB34378.1; -

DR: EMBL; ECO01156; AAH11656.1; -

DR: PIR; I12835; I52835.

DR: Genew; HGNC:1728; CDC27.

DR: GR; P3260; -

DR: NIM; 116946; -

DR: GO; GO:0005813; C:centrosome; TAS.

DR: GO; GO:0005819; C:spindle; TAS.

DR: GO; GO:0008283; F:cell proliferation; TAS.

DR: GO; GO:0007091; F:mitotic metaphase/anaphase transition; TAS.

DR: InterPro; IPR001440; TPR.

DR: Pfam; PF00515; TPR; 8.

DR: SMART; SM00028; TPR; 8.

KW: Repeat; TPR repeat; Nuclear protein; Polymorphism.

REPEAT 84 114 TPR 1.

FT REPEAT 84 114 TPR 1.

FT REPEAT 115 148 TPR 2.

FT REPEAT 499 532 TPR 3.

FT REPEAT 567 600 TPR 4.

FT REPEAT 602 634 TPR 5.

FT REPEAT 635 668 TPR 6.

FT REPEAT 670 702 TPR 7.

FT REPEAT 704 736 TPR 8.

FT REPEAT 737 770 TPR 9.

FT VARIANT 496 496 Y-> H (IN dbSNP:136666).

FT CONFLICT 319 319 /PTId=VAR_014489.

FT CONFLICT 403 403 K-> KTPRVLQ (IN REF. 3).

FT CONFLICT 460 460 K-> E (IN REF. 3).

FT CONFLICT 715 715 MISSING (IN REF. 1).

SEQ SEQUENCE 824 AA; 91867 NW; E6C8FF9C1BFDCA CR64;

Query Match 48.8%; Score 59; DB 1; Length 824;

Best Local Similarity 54.5%; Pred. No. 0.071; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 LQLARRYLNSQASAYVILK 24

Db 41 LFLLATCYRSGRAYKAVRLKLK 62

RESULT 2

BINA_ELEMENT STANDARD; PRT; 806 AA.

ID_BIMA_ELEMENI STANDARD; PRT; 806 AA.

AC_P1785; 01-AUG-1992 (Rel. 23, Created)

DT_01-AUG-1992 (Rel. 23, Last sequence update)

DT_16-OCT-2001 (Rel. 40, Last annotation update)

DE_Protein_bima.

GN_Nidulans (Aspergillus nidulans).

OS_Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericellales.

OC_NCBI_TaxID=162425;

CX_RN_SEQUENCE FROM N.A.

RP_STRAIN=R153;

RX_MEDLINE=2121243; PubMed=1170001;

RA_O'Donnell K.L., Osmanni A.H., Osmanni S.A., Morris N.R.;

RT_bima encodes member of the tetratricopeptide repeat family of proteins and is required for the completion of mitosis in Aspergillus nidulans".

RT_J. Cell Sci. 99:711-719(1991).

RL_- FUNCTION: REQUIRED FOR THE COMPLETION OF MITOSIS IN ASPERGILLUS

NIDULANS SUBCELLULAR LOCATION: Nuclear (Potential).

SIMILARITY: BELONGS TO THE CDC27/NUC2 FAMILY.

SIMILARITY: Contains 8 TPR repeats.

SIMILARITY: Contains 8 TPR repeats.

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EMBL; X59269; CRAA1959.1; -

DR: PIR; A53256; A53256.

DR: InterPro; IPR001440; TPR.

DR: Pfam; PF00515; TPR; 7.

DR: SMART; SM00028; TPR; 7.

DR: Cell division; Cell cycle; Mitosis; Repeat; TPR repeat; Nuclear protein.

KW_Nuclear protein.

FT REPEAT 76 109 TPR 1.

FT REPEAT 127 160 TPR 2.

FT DOMAIN 260 399 BINA_DOMAIN.

FT REPEAT 513 546 TPR 3.

FT REPEAT 581 614 TPR 4.

FT REPEAT 616 648 TPR 5.

FT REPEAT 649 682 TPR 6.

FT REPEAT 684 716 TPR 7.

FT REPEAT 751 784 TPR 8.

SQ_SEQUENCE 806 AA; 89714 NW; F137BDE3A74C0457 CRC64;

Query Match 38.0%; Score 46; DB 1; Length 806;

Best Local Similarity 56.2%; Pred. No. 10;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 LLARYLNSQASAY 20

Db 48 LLALCYLQNGQVKAW 63

RESULT 3

YG22_HAEIN STANDARD; PRT; 161 AA.

ID_YG22_HAEIN STANDARD; PRT; 161 AA.

AC_P4475; 01-NOV-1995 (Rel. 32, Created)

AC_P4475; 01-NOV-1995 (Rel. 32, Last sequence update)

AC_P4475; 28-FEB-2003 (Rel. 41, Last annotation update)

AC_P4475; DE_Hypothetical Protein Hil622 precursor.

GN_Hil622.

OS_Haemophilus influenzae.

OC_Bacteria/Proteobacteria/Gammaproteobacteria; Pasteurellales;

OC_Bacteriophages/Bacmophilus.

NCBI_TaxID=727;

OX_OX_SEQUENCE FROM N.A.

RN_RP_STRAIN=Rd / K920 / ATCC 51907;

RC_RC_MEDLINE=535030; PubMed=7512800;

RX_RX_Fleischmann R.-D., Adams M.-D., White O., Clayton R.-A., Kirkness E.-F., Kerlavage A.-R., Bult J.-F., Dougherty B.-A., Merrick J.-M., McKenney K., Sutton G., Fitzhugh W.-W., Fields C.-A., Gocayne J.-D., Scott J.-D., Shirley R.-L., Liu L.-L., Glodek A., Kelley M.-J., Weidman J.-F., Phillips C.-A., Spriggs T.-R., Hedbom E., Cotton M.-D., Utterback T.-R., Hanna M.-C., Nguyen D.-T., Saudek D.-M., Brandon R.-C., Fine L.-D., Fritchman J.-J., Fuhrman J.-J., Geoghegan N.-S.-M., Gneh C.-L., McDonald L.-A., Small K.-V., Fraser C.-M., Smith H.-O., Ventur J.-C., RN_RP_RT_RT_RL_RL_Science 269:496-512(1995).

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CC EMP1; U32835; AAC23271.1; -.

CC P1P; F66038; F64038.

CC TIGR; HU1622; -.

CC HYPOTHEICAL PROTEIN; Transmembrane; Signal; Complete proteome.

CC KW OR 21 (POTENTIAL).

CC SIGNAL 1 23

CC CHAIN 24 161 HYPOTHETICAL PROTEIN HU1622.

CC TRANSMEM 129 149 POTENTIAL.

CC SEQUENCE . 161 AA; 17520 MW; C930AA13F25D36 CRC64;

CC SQ

Query	Match	Score	DB	Length	DB	Gaps
Best Local Matches	Similarity	37.2%	45	1	161	0;
8;	Conservative	50.0%	Prdt. No.	2.4		
Mismatches			3;	Mismatches	5	
				Indels	0;	

Qy 5 LLARCYLNSQASAY 20

Db 10 LFACYLNAYAFLY 25

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EMBL; PTB; M2AN088; M2AN085
DR

Query	Match	Score	DB	Length
Wolmerp, Koen	LEOZB .			
InterPro; IPR05533; AMOP.				
InterPro; IPR03886; Nidogen_ext.				
Pfam; PF03782; AMOP;				
SMART; SM0723; AMOP;				
SMART; SM0539; NIDO_1.				
Hypothetical protein; Transmembrane				
SEQUENCE 1459 AA; 16594 MW;	789014C5599513C4 CRC64;			
SQ				
Best Local Matches	37.2%; 7;	Score 45; Conservative	DB 1; Pred. No. 29;	Length 145
Indels	Mismatches		3;	

RESULT 5

ID	SAS3 YEAST	STANDARD:	ERT;	831 AA.
AC	P34218 ;	(Rel. 28, Created)		
DT	01-FBB-1994	(Rel. 28, Last sequence update)		
DT	01-FBB-1994	(Rel. 28, Last annotation update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DB	SAS3 Protein			
GN	SAS3 OR YBL052C OR YBL0515 OR YBL0507.			
OS	Saccharomyces cerevisiae (Baker's Yeast)			
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces			
OX	NCBI_TaxID=4932 ;			
[1]				
RN		SEQUENCE FROM N.A.		
RP		STRAN=S28C;		
RC		MEDLINE=8154187;		
RX		Scheipers B., el Bakkoury M., Vizirdeels P.,		
RA		"Sequencing and functional analysis of a 32'		
RA		left arm of yeast chromosome II. Identification of genes."		
RT		frames, including the KIP1 and SEC17 genes."		
RT		yeast 9:1355-1371(1993).		
[2]				
RP		CHARACTERIZATION		
RP				

RA REILLYNDER C., LOWELL J., CLARKE A., PILLUS L.;
RT "Yeast SAS silencing genes and human genes associated with AML and
HIV-1 Tat interactions are homologous with acetyltransferases.";
RT Nat. Genet. 14:42-49(1996).
RL [3]
RN
RP ERRATUM.
RX MEDLINE=97285133; PubMed=91040406;
RA Reillyndyer C., Lowell J., Clarke A., Pillus L.;
RL Nat. Genet. 16:109-109 (1997).
CC -1- FUNCTION: INVOLVED IN SILENCING THE HMR LOCUS.
CC -1- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR	EMBL: Z35814;	GO:00084873	-;	
DR	PIR: S39835;	S39835		
DR	SGD: S0000148;	SAS3.		
DR	GO: GO:0016407;	P:acetyltransferase activity; IDA.		
DR	GO: GO:0016568;	P:chromatin modification; IMP.		
DR	GO: GO:0008347;	P:chromatin silencing at HML and HMR (senso stricto); IMP.		
DR	GO: GO:0008348;	P:chromatin silencing at telomere; IMP.		
DR	InterPro: IPR002717;	MOZ SAS		
DR	InterPro: IPR001087;	Znf-C2H2.		
DR	Pfam: PF01853;	MOZ_SAS; I.		
DR	Pfam: PF00096;	zf-C2H2; 1.		
KW	Zinc-finger.			
FT	ZN FING	301	323	C2HC-TYPE.
FT	DOMAIN	736	831	ASP/Glu-RICH (ACIDIC).
FT	SEQUENCE	831 AA:	97582 MW;	ACFB51B225CB4A71 CRC64;
Qy	Query Match	36.8%	Score 44.5;	DB 1; Length 831;
Qy	Best Local Similarity	37.0%	Pred. No. 18;	
Qy	Matches 10;	Conservative	6; Mismatches	
Qy			6;	Indels 5; Gaps 1;
Qy	2 NLQLLARCYLSNSQAY----SAYYL 23			
Db	355 NLCLIAKCFINSKTLVYDVEPPLFYIL 381			

PSD3 CAEEL
ID PSD3 CAEEL
STANDARD;
PRT; 504 AA.
AC Q04908;

DT	01-FEB-1994 (Rel. 28, Created)	GN	SPBC23B6-09.
DT	01-FEB-1994 (Rel. 28, Last sequence update)	OS	Schizosaccharomyces pombe (Fission yeast).
DE	Probable 26S Proteasome non-ATPase regulatory subunit 3.	OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
GN	RPN 3 OR C50C11.2.	OC	Schizosaccharomyces.
OC	Caenorhabditis elegans.	OC	NCBI_TaxID=1866,
OC	Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	RN	[1]
OX	Caenorhabditidae; Pejodoridae; Caenorhabditis.	RC	SEQUENCE FROM N.A.
OX	NCBI_TaxID=6239;	RX	STRAIN=912;
RN	[1]	RX	MEDLINE=21848401; PubMed=11859360;
RP	SEQUENCE FROM N.A.	RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyte R., Stewart A., Baker S., Bowman S., Hayles J., Baker S., Basham D., Churcher C.M., Peat N., Chillingworth T., Churcher C.M., Brown D., Brown S., Collins M., Connor R., Cronin M., Davis P., Feltwell T., Fraser A., Gillees S., Gillee A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jakes K., Jones L., Jones M., Leathem S., McDonald S., McLean J., Mooney P., Moule S., Mongail K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkertaert G., Aert R., Robben J., Grymonprez B., Weljens I., Vansstreels B., Rieger M., Schaefer M., Mueller-Auer S., Fuchs M., Fritze C., Holzer E., Hilbert H., Reinhardt R., Pohl T.M., Pohl C., Ringer I., Beck A., Lehrach H., Wambutt R., Purnelle B., Egger P., Zimmermann W., Wedler H., Gofeau A., Dreano S., Gloux S., Lejaire V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Roche M., Gaillardin C., Talleda V.A., Garzon A., Theude G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe." Nature 415:871-880(2002). [2]
RR	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."	RN	SEQUENCE OF 633-836 FROM N.A., AND SUBCELLULAR LOCATION.
RR	RPTD=968 h96;	RX	MEDLINE=2022368; PubMed=10759889;
CC	-1- FUNCTION: ACTS AS A REGULATORY SUBUNIT OF THE 26 PROTEASOME WHICH IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS (BY SIMILARITY).	RA	Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T., Hirakawa Y.,
CC	-1- SUBUNIT: THE 26S PROTEASOME IS COMPOSED OF A CORE PROTEASE, KNOWN AS THE 20S PROTEASOME, CAPPED AT ONE OR BOTH ENDS BY THE 19S REGULATORY COMPLEX (RC). THE RC IS COMPOSED OF AT LEAST 18 DIFFERENT SUBUNITS IN TWO SUBCOMPLEXES, THE BASE AND THE LID, WHICH FORM THE PORTIONS PROXIMAL AND DISTAL TO THE 20S PROTEOLYTIC CORE, RESPECTIVELY (BY SIMILARITY).	RT	"Large-scale screening of intracellular protein localization in living fission yeast cells by the use of GFP-fusion genomic DNA library." Genes Cells 5:169-190(2000).
CC	-1- DOMAIN: CONTAINS 1 PCI DOMAIN.	RL	! - SUBCELLULAR LOCATION: Nuclear, and cytoplasmic.
CC	-1- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S3 FAMILY.	CC	-1- SIMILARITY: Contains 9 TPR repeats.
CC	[2]	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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DR	EMBL; I09634; AAA27966.1; -.	DR	EMBL; AB027111; BA87215.1; -.
DR	PTR; S44783; S44783.	DR	InterPro; IPR0000717; PC1.
DR	WormPep; C30C11.22; CE00101.	DR	PFam; PF001399; PC1; 1.
DR	InterPro; IPR0000717; PC1.	DR	SMART; SM00088; PINT; 1.
DR	Pfam; PF001399; PC1; 1.	KW	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;
DR	SMART; SM00088; PINT; 1.	FT	Query Match 36.4%; Score 44; DB 1; Length 504;
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Best Local Similarity 50.0%; Pred. No. 13;
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	InterPro; IPR001440; TPR.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
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DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
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DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	SEQUENCE 504 AA; 57506 NW; 062E476685PCDA07 CRC64;	FT	Repeat; TPR repeat; Nuclear protein GLN-RICH.
DR	Matches 9; Conservative 3;		

RA Newman A.K., Rubin R.A., Kim S.-H., Modrich P., Modrich P.; "DNA sequences of structural genes for Eco RI DNA restriction and RT modification enzymes"; J. Biol. Chem. 256:2131-2139 (1981).

[3] CONFIRMATION OF AMINO AND CARBOXYL ENDS OF SEQUENCE BY AMINO ACID ANALYSIS; MEDLINE=1117319; PubMed=6557702;

RA Rubin R.A., Modrich P., Varmanian T.C.; "Partiai NH₂ and COOH-terminal sequence analyses of Eco RI DNA restriction and modification enzymes"; J. Biol. Chem. 256:2140-2142 (1981).

-!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GAATTC, CAUSES SPECIFIC METHYLATION ON A-3 ON BOTH STRANDS, AND PROTECTS THE DNA FROM CLEAVAGE BY THE ECORI ENDONUCLEASE.

-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-adenosyl-L-homocysteine + DNA 6-methylaminopurine.

-!- SUBUNIT: Monomer.

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DR EMBL; XLS828; CAC16944.1; -.

RA InterPro; IPR001988; Caulimo coat.

RT InterPro; IPR001878; Znf_CCHC.

RL PFAM; PF00982; zf-CCHC_1.

CC PRINTS; PR00939; C2HC2NFGFR.

CC PRINTS; PR00221; CAULIMOCAOT.

CC SMART; SM03431; ZNF_C2HC_1.

CC PROSITE; PS50158; ZF_CCHC_1.

CC Coat Protein; Zinc-finger.

CC ZN FING; 381 398 CCHC-TYPE.

CC SEQUENCE 441 AA; 52102 NW; 07244CD2181CF4FF CRC64;

Query Match 35.5%; Score 43; DB 1; Length 441;

Best Local Similarity 39.1%; Pred. No. 16;

Matches 9; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 VNLQLIARCYLSN-SQAYSAYY 21

Db 216 INLECNMCYLENPCFEFQSYV 238

RESULT 12

TI160_HUMAN STANDARD PRT; 513 AA.

ID TI160_HUMAN Q9BWK7; AC Q92933; Q95624; Q13430; Q9BWK7; DT 15-JUL-1998 (Rel. 36, Created)

KW Chinnadurai G.; Subramanian T., Coleman D., Kamine J., Elangovan B., Subramanian T., Coleman D., Chinnadurai G.; Subramanian T., Coleman D., DT 15-SEP-2003 (Rel. 42, Last sequence update)

FT "Identification of a cellular protein that specifically interacts with the essential cysteine region of the HIV-1 Tat transactivator.";

FT 60 kDa Tat interactive protein (Tip60) (HIV-1 Tat interactive protein (Tip60)) (HIV-1 Tat interacting protein (cPLA2) interacting protein).

FT ATAPIP OR TI60.

FT Homo sapiens (Human).

FT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FT NCBI_TAXID=9606;

RN [1] - TAXID=9606;

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lymphoblast; MEDLINE=96182337; PubMed=8607265;

RX Kamine J., Elangovan B., Subramanian T., Coleman D., Chinnadurai G.; Subramanian T., Coleman D., Chinnadurai G.; Subramanian T., Coleman D., DT 15-SEP-2003 (Rel. 42, Last sequence update)

RA Sheridan A.M., Force T., Yoon H.-J., O'Leary E., Choukroun G., Taheri M.R., Bonventre J.V., RA Sheridan A.M., Force T., Yoon H.-J., O'Leary E., Choukroun G., RA Taheri M.R., Bonventre J.V., RA Sheridan A.M., Force T., Yoon H.-J., O'Leary E., Choukroun G., RA Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K., Altzhausen R.D., Collins F.S., Wagner L., Shemer C.M., Schuler G.D., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Scheetz T.E., RA

RESULT 11

COAT_SOCMV STANDARD PRT; 441 AA.

ID COAT_SOCMV AC P15627; DT 01-APR-1990 (Rel. 14, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Coat protein.

GN IV.

OS soybean chlorotic mottle virus.

OC Viruses; Retroviridae; Caulimoviridae;

OC soybean chlorotic mottle-like viruses.

OX NCBI_TAXID=10651;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=90098857; PubMed=2602148;

RX REVISIONS.

RA Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

RA RA Hasegawa A., Verver J., Shimada A., Saito M., Hibi T., van Kammen A., Miki K., Kamiya-Iwaki M., Goldbach R., RA RA "The complete sequence of soybean chlorotic mottle virus DNA and the identification of a novel promoter." Nucleic Acids Res. 17:9933-10013(1989).

RN [2]

RX TISSUE=Cervix; MEDLINE=2238827; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shemer C.M., Schuler G.D., RA Altzhausen R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Scheetz T.E., RA

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueline A., Peters G.J., Abramson R.D., Mulhall S.J., Bosak S.A., McEwan P.J., McKernan K.H., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fabey J., Helton E., Kerrest M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Bouffard G.G., Rodriguez R.W., Touché J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnearch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [4]

QY	2 NQLLACQYLSQAY 17 : : : : 315 NCLLARCFLDHKTLV 330			
RESULT 13				
VIB04_VACCC	STANDARD;	PRT;	558 AA.	
ID P210701;				
AC P210701;				
DT 01-FEB-1991 (Rel. 17, Created)				
DT 01-FEB-1991 (Rel. 17, Last sequence update)				
DT 16-OCT-2001 (Rel. 40, Last annotation update)				
DE Protein B4.				
GN Vaccinia virus (strain Copenhagen).				
OS dsDNA viruses, no RNA stage; Chordopoxvirinae;				
CC Viruses;				

OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE:9101027; PubMed=221972;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
PA Paolletti E.;
RA

"The complete DNA sequence of vaccinia virus.";
R.T. Winslow J.P.,
Virology 173:247-266 (1990).
[2]
RN
COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paetzel E.;
PR "Appendix to 'The complete DNA sequence of vaccinia virus'";
Virology 173:517-563 (1990).
RL

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CC or send an email to license@ibd-sid.cn).

EMBL; M35027; AA48200.1; - .
DR; C42526; C42526.
DR; InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 6.
SMART; SM00248; ANK; 4.
PROSITE; PS56099; ANK_REPEAT; 1;
PROSITE; PS56100; ANK_ANCHOR; 1;
PROSITE; PS56101; ANK_ANCHOR; 1;

LUR	PROLINE; PS55-29/;	ANK; RLF; REGION;	1.
KW	LATE PROTEIN;	REPEAT; ANK - REPEAT;	
FT	REPEAT	65	95
FT	REPEAT	169	205
FT	REPEAT	209	239
FT	REPEAT	243	272
FT	REPEAT	276	304
FT	REPEAT	339	368
FT	REPEAT	352	380
FT	REPEAT	352	380

```

    REPEAT      3/2      4UL      MM;      ANA /;
    SEQ        558 AA:  ED67F454DB7FC76 CRC64;
    Query Match      35.5%      Score 43;      DB 1;      Length 558;
    Best Local Similarity 22.7%;      Fred. No. 21;
    Matches 5;      Conservative 7;      Mismatches 10;      Indels 0;
    Gaps 1
    QY        3 LOLLARCLNSNSAYSAYWILK 24

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein B4.

GN Vaccinia virus (strain WR), RNA stage; Poxviridae; Chordopoxvirinae;
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

NCBI_TAXID=10254;

[1]

RN SEQUENCE FROM N.A.
MEDLINE=1125063; PubMed=2045793;
RX Howard S.T., Chan Y.S., Hwang S.T.;
RA "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
the right inverted terminal repeat.";
RT J. Gen. Virol. 72:1349-1376(1991).;

[2]

RP SEQUENCE FROM N.A.
RX MEDLINE=11111982; PubMed=1846491;
RA Howard S.T., Chan Y.S., Smith G.L.;
RT "Vaccinia virus homologues of the Shope fibroma virus inverted
terminal repeat proteins and a discontinuous ORF related to the tumor
necrosis factor receptor family.";
RL Virology 180:633-647(1991).;

-; SIMILARITY: Contains 7 ANK repeats.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; D11079; BAA01834.1; -;
EMBL; M85055; AAA41965.1; -;
DR PIR; JQ1798; JQ1798;
DR InterPro; IPR02110; ANK.
DR PF00023; anki_6.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50397; ANK REP_REGION; 1.
KW Late protein; Repeat; ANK repeat.
FT REPEAT 65 95 ANK 1.
FT REPEAT 169 205 ANK 2.
FT REPEAT 209 239 ANK 3.
FT REPEAT 243 272 ANK 4.
FT REPEAT 276 304 ANK 5.
FT REPEAT 339 368 ANK 6.
FT REPEAT 372 401 ANK 7.
SQ SEQUENCE 558 AA; 65453 MW; 10089DF5FB1ABF0 CRC64;

Query Match 35.5%; Score 43; DB 1; Length 558;
Best Local Similarity 22.7%; Score 20; No. 21; Indels 0; Gaps 0;
Matches 5; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

SYL_ARCFU STANDARD; PRT; 932 AA.

ID SYL_ARCFU

AC O3050;

DT 15-TUL-1998 (Rel. 36, Created)

DT 15-TUL-1998 (Rel. 36, Last sequence update)

DT 28-PER-2003 (Rel. 41, Last annotation update)

DE Leucine-tRNA synthetase (EC 6.1.1.4) (Leucine-tRNA ligase) (Leurs).

GN AF4242.

OS Archaeoglobus fulgidus.

Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobus;

NCBI_TAXID=2234;

[1]

SEQUENCE FROM N.A.
RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RC RX MEDLINE=9804943; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

OC Kyrides N.C., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrides N.C.,

NC Fiebschmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirchner E.F., Dougherty B.A., McKerney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Socayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cottrell P.W., Springs T., Ariach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., DiAndrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.,

RA "The complete genome sequence of the hyperthermophilic, sulphate-

reducing archaeon Archaeoglobus fulgidus.";

RT reducing archaeon Archaeoglobus fulgidus.";

RL SEQUENCE FROM N.A.
RX MEDLINE=364-370(1997); ATP + L-leucine + tRNA(Leu) = AMP +

RT diphosphate + L-leucyl-tRNA(Leu).

CC -; SUBCELLULAR LOCATION: Cytoplasmic.

CC -; SIMILARITY: Belongs to Class-I aminoacyl-tRNA synthetase family.

CC ---

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or send an email to license@isb-sib.ch).

CC ---

CC DR EMBL; AB01108; AAB01241.1; -.

DR PIR; F69552; F69552.

DR TIGR; AF2421; -.

DR HAMAP; MF_0009; -; 1.

DR InterPro; IPR004493; Leu-tRNA-syntia.

DR InterPro; IPR002300; tRNA-synt_1a.

DR InterPro; IPR001412; tRNA-synt_1.

DR Pfam; PF00133; tRNA-synt_1.

DR TIGRFAMS; TIGRF00395; leu_arch; 1.

DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW Complete proteome.

FT SITE 38 48 "HIGH" REGION.

FT SITE 630 634 "XMSX" REGION.

FT BINDING 633 633 ATP (BY SIMILARITY).

FT SEQUENCE 932 AA; 108628 MW; 8544E93ED674D2BA CRC64;

Query Match 35.5%; Score 43; DB 1; Length 932;

Best Local Similarity 69.2%; Pred. No. 37; 1; Mismatches 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 LSNSQAYASAYIL 23

DB 516 LSDSTIYMAYIL 528

Search completed: February 2, 2004, 12:47:12

Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM Protein - protein search, using sw model

Run on: February 2, 2004, 09:20:42 ; Search time 177 Seconds

(without alignments)

34.990 Million cell updates/sec

Title: US-10-036-492-6

Perfect score: 121

Sequence: 1 VNQLIARCVLSNSQAYSAYVILK 24

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebr:ate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaeap:*

SPREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebr:ate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaeap:*

SPREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebr:ate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaeap:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebr:ate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	75.2	471	10 QBWMB	QBWMB arabidopsis
2	91	75.2	744	10 QBLK91	QBLK91 mus musculus
3	59	48.8	394	11 QBR568	QBR568 mus musculus
4	59	48.8	399	11 QBX715	QBX715 escherichia
5	53	43.8	795	16 QBY005	QBY005 turkey aden
6	52	43.0	300	12 QBPBL6	QBPBL6 metagonimus
7	49	40.5	146	5 QBDUB0	QBDUB0 streptococc
8	49	40.5	262	16 QBDUB0	QBDUB0 streptococc
9	49	40.5	875	5 QD4C21	QD4C21 drosophila
10	49	40.5	900	5 Q9VS37	Q9VS37 drosophila
11	48	39.7	501	5 Q19498	Q19498 caenorhabdi
12	47	38.8	298	16 Q97GR8	Q97GR8 clostridium
13	47	38.8	758	5 Q8IAY2	Q8IAY2 plasmidium
14	46.5	38.4	7149	5 Q8IM09	Q8IM09 plasmidium
15	46	38.0	173	17 Q8P958	Q8P958 pyrococcus
16	46	38.0	300	10 Q39979	Q39979 hyoscyamus

17	46	36.0	332	10 QBL719	QBL719 arabidopsis
18	46	36.0	437	10 Q9M1D6	Q9M1D6 arabidopsis
19	46	441	436	4 Q8N7G5	Q8N7G5 homo sapien
20	46	38.0	453	10 Q9FVU2	Q9FVU2 lycoopersico
21	46	38.0	454	10 QBLK91	QBLK91 arabidopsis
22	46	38.0	458	10 QBL727	QBL727 arabidopsis
23	46	38.0	462	10 QBL782	QBL782 arabidopsis
24	46	38.0	520	10 Q9X978	Q9X978 hyoscyamus
25	46	38.0	549	10 Q9XJ25	Q9XJ25 solanum tub
26	46	38.0	549	10 Q9XJ25	Q9XJ25 solanum tub
27	46	38.0	550	10 Q9SBU0	Q9SBU0 solanum tub
28	46	38.0	551	10 Q9ZTQ6	Q9ZTQ6 caenorhabdi
29	46	38.0	552	5 Q8MQB6	Q8MQB6 caenorhabdi
30	46	38.0	553	10 Q9ATN6	Q9ATN6 capsicum an
31	46	38.0	556	10 Q9XJ32	Q9XJ32 solanum tub
32	46	38.0	556	10 Q9ZTQ7	Q9ZTQ7 solanum tub
33	46	38.0	557	10 Q9ZTQ8	Q9ZTQ8 solanum tub
34	46	38.0	574	5 Q95QT8	Q95QT8 canorhabdi
35	46	38.0	582	6 Q9GM29	Q9GM29 macaca fasc
36	46	38.0	724	6 Q9SJZ1	Q9SJZ1 macaca fasc
37	46	38.0	882	4 QBN02	QBN02 homo sapien
38	46	38.0	1145	12 Q9IV56	Q9IV56 olive latent
39	46	38.0	1164	17 Q8P958	Q8P958 methanosa
40	46	38.0	1320	4 QBNDBW8	QBNDBW8 homo sapien
41	46	38.0	1772	5 Q9W040	Q9W040 drosophila
42	45	37.2	455	3 Q08231	Q08231 sacharomyces
43	45	37.2	508	5 Q9BL61	Q9BL61 canorhabdi
44	45	37.2	527	16 QBFON0	QBFON0 leptospira
45	45	37.2	759	2 Q93M42	Q93M42 streptococc

ALIGNMENTS

RESULT 1					
QBW4MB	ID	QBW4MB	PRELIMINARY	PRT	PRT ;
AC	AC	AC	PRELIMINARY ;	471 AA.	
DT	DT	DT	(TRMBLrel; 20, Created)		
DT	DT	DT	(TRMBLrel; 20, Last sequence update)		
DT	DT	DT	(TRMBLrel; 22, Last annotation update)		
DE	DE	DE	CDC27/NUC2-like protein		
GN	GN	GN	AT2G20000, T2C17, 20 QR Am2G20000.		
OS	OS	OS	Arabidopsis thaliana (Mouse-ear cress)		
RA	RA	RA	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
RA	RA	RA	Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; OC		
RA	RA	RA	eurosid II; Brassicaceae; Brassicaceae; Arabidopsis ;		
RN	RN	RN	[1] N		
RP	RP	RP	SEQUENCE FROM N.A.		
RA	RA	RA	Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,		
RA	RA	RA	Palm C.J., Bowser L., Jones T., Barth J., Carninci P., Chen H.,		
RA	RA	RA	Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,		
RA	RA	RA	Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,		
RA	RA	RA	Sakurai T., Satou M., Seki M., Shirin P., Yamada K., Shinozaki K.,		
RA	RA	RA	Ecker J., Theologis A., Davis R.W.; [2]		
RL	RL	RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
RN	RN	RN			

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	75.2	471	10 QBWMB	QBWMB arabidopsis
2	91	75.2	744	10 QBLK91	QBLK91 mus musculus
3	59	48.8	394	11 QBR568	QBR568 mus musculus
4	59	48.8	399	11 QBX715	QBX715 escherichia
5	53	43.8	795	16 QBY005	QBY005 turkey aden
6	52	43.0	300	12 Q9BPBL6	Q9BPBL6 metagonimus
7	49	40.5	146	5 QBDUB0	QBDUB0 streptococc
8	49	40.5	262	16 QBDUB0	QBDUB0 streptococc
9	49	40.5	875	5 QD4C21	QD4C21 drosophila
10	49	40.5	900	5 Q9VS37	Q9VS37 drosophila
11	48	39.7	501	5 Q19498	Q19498 caenorhabdi
12	47	38.8	298	16 Q97GR8	Q97GR8 clostridium
13	47	38.8	758	5 Q8IAY2	Q8IAY2 plasmidium
14	46.5	38.4	7149	5 Q8IM09	Q8IM09 plasmidium
15	46	38.0	173	17 Q8P958	Q8P958 pyrococcus
16	46	38.0	300	10 Q39979	Q39979 hyoscyamus

Query Match 75.2% ; Score 91 ; DB 10 ; Length 471 ;
Best Local Similarity 75.0% ; Pred. No. 1.8e-06 ;

DR	EMBL; AP002551; BAB33726_1; ALT_INIT.	
DR	InterPro; IPR006500; Primase_C.	
DR	InterPro; IPR006154; Toprim_sub.	
DR	SMART; SM00493; TOPRIM; 1.	
DR	TIGRFAM; TIGR01613; primase_Cterm; 1.	
DR	Complete proteome.	
RW	TIGRFAM; TIGR01613; primase_Cterm; 1.	
SEQUENCE	796 AA;	87237 MW;
Qy	1 VNLQLI---ARCVLNSNQSYASAYILK 24	5A6BE08B6020A672 CRC64;
Matches	10; Conservative 8; Mismatches 6;	Indels 4; Gaps 1;
Db	193 VNLQLINANGGKCPFLKGQVNAFVVE 220	
RESULT 6		
ID	Q9YUQS	PRELIMINARY;
AC	Q9YUQS;	PRT;
DT	01-MAY-1999 (TREMBLrel. 10, Created)	300 AA.
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	E3 protein.	
GN		
CS	Turkey adenovirus 3.	
CC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Siadenovirus.	
CX	NCP_ TaxID=41678;	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE=990093844; PubMed=9791022;	
RX	Virology 249:307-315(1998).	
RN	"The complete DNA sequence and genome organization of the avian	
RA	adenoivirus, hemorrhagic enteritis virus."	
RA	pitcovski J., Mualem M., Rei-Koren Z., Krispel S., Gallili G.,	
RA	Michael A., Goldberg D.;	
RA	"The complete DNA sequence and genome organization of the avian	
RT	adenoivirus, hemorrhagic enteritis virus."	
RT	Virology 249:307-315(1998).	
RN	SEQUENCE FROM N.A.	
RA	pitcovski J., Mualem M., Rei-Koren Z., Krispel S., Gallili G.,	
RA	Michael A., Goldberg D.;	
RA	"The complete DNA sequence and genome organization of the avian	
RA	adenoivirus, hemorrhagic enteritis virus."	
RA	Virology 249:307-315(1998).	
[2]		
RN	SEQUENCE FROM N.A.	
RA	pitcovski J., Mualem M., Rei-Koren Z., Krispel S., Gallili G.,	
RA	Michael A., Goldberg D.;	
RA	"The complete DNA sequence and genome organization of the avian	
RA	adenoivirus, hemorrhagic enteritis virus."	
RA	Virology 249:307-315(1998).	
RN	SEQUENCE FROM N.A.	
RA	pitcovski J., Mualem M., Rei-Koren Z., Krispel S., Gallili G.,	
RA	Michael A., Goldberg D.;	
RA	"The complete DNA sequence and genome organization of the avian	
RA	adenoivirus, hemorrhagic enteritis virus."	
RA	Virology 249:307-315(1998).	
Qy	1 VNLQLIARCVLNSNQSYASAYILK 24	Score 52; DB 12; Length 300;
Matches	10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	
Db	216 VNPLCISNCFKGNSDCAFVICK 239	
RESULT 7		
ID	Q9BP16	PRELIMINARY;
AC	Q9BP16;	PRT;
DT	01-JUN-2001 (TREMBLrel. 17, Created)	146 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	Cysteine proteinase (Fragment).	
GN		
CS	Metagonimus yokogawai.	
CC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;	
CC	Opisthorchiida; Opisthorchiida; Opisthorchiida; Heterophyidae;	
CC	Metagonimus.	
NCBI_TaxID	84529;	
RN	SEQUENCE FROM N.A.	
RA	Park H., Yun H.C., Kim K.Y., Park S.Y., Park S.K.;	
RA	"Metagonimus yokogawai cysteine proteinase (NYCP4, mRNA.)"	
RA	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.	
RESULT 8		
Q8DJB0	OBDDUBO	PRELIMINARY;
AC	OBDDUBO;	PRT;
DT	01-MAR-2003 (TREMBLrel. 23, Created)	262 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	Putative ABC transporter, permease protein.	
GN		
OS	Streptococcus mutans.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCTC TaxID=1309;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RC	STRAIN=UA159 / ATCC 700610 / Serotype C;	
RX	Medline=2225063; PubMed=12397186.	
RA	Ajdic D., McShan W.M., McNaughlin R.E., Savic G., Chang J.J.,	
RA	Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,	
RA	Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Farretti J.J./	
RT	"Genome sequence of Streptococcus mutans UA159, a cariogenic dental	
RT	pathogen."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).	
DR	EMBL; AB014945; AACN8765.1.;	
KW	Complete proteome.	
SQ	SEQUENCE 262 AA;	29142 MW; 7C236A590BD03C532 CRC64;
Qy	1 UNIQLLARCVLNSNQSYASAYILK 22	Score 49; DB 16; Length 262;
Matches	11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;	
Db	137 MGGLDLALVLUCKSKFDFFDAYI 158	
RESULT 9		
Q24021	PRELIMINARY;	PRT;
AC	Q24021;	875 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
DE	CD027DM,	
GN	CG027 OR CG8610.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydriidae; Drosophilidae; Drosophila.	
OX	NCTC TaxID=127;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

RA	Tugendreich S., Thesis (1995), Johns Hopkins University.	Science 287:2185-2195(2000); EMBL; AB003559; AAF5592.1; -.
RA	DRB; U18288; AAA57340.1; -.	DR FlyBase; FBgn0012058; Cdc27.
RA	InterPro; IPR001440; TPR.	DR InterPro; IPR001440; TPR.
RA	Pfam; PF00015; TPR; 6.	DR Pfam; PF00015; TPR; 6.
RA	SMART; SM00028; TPR; 5.	DR SMART; SM00028; TPR; 6.
RA	SEQUENCE 875 AA; 97658 MW; 37662A8843FP39FD CRC64;	SQ SEQUENCE 900 AA; 101284 MW; 363333789A783464 CRC64;
Qy	Query Match Score 49; DB 5; Length 900; Best Local Similarity 45.0%; Pred. No. 27; Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	Query Match Score 49; DB 5; Length 900; Best Local Similarity 45.0%; Pred. No. 27; Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Db	5 LLARCYLSNSQAYSAYILK 24 42 LLATSYFRRSNQVHQAYNLLK 61	Qy 5 LLARCYLSNSQAYSAYILK 24 Db 42 LLATSYFRRSNQVHQAYNLLK 61
RESULT 11		
Q9VS37	PRELIMINARY; PRT; 900 AA.	Q19498 PRELIMINARY; PRT; 501 AA.
ID	AC Q9VS37; 13 Created)	ID Q19498; 01, Created)
AC	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	AC DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	DE HYPOTHETICAL 56.8 kDa protein.
DE	CDC27 Protein.	GN F16H11.1.
GN	Drosophila melanogaster (Fruit fly).	OS Caenorhabditis elegans.
OS	Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.	OC Rhabditidae; Peleodirina; Caenorhabditis.
OC	OC OX NCBI_TaxID=6239;	OX NCBI_TaxID=6239;
OC	OC RN [1]; STRAIN=BRI227;	RN SEQUENCE FROM N.A.
OC	RP RC STRAIN=BRI227;	RC STRAIN=Bristol N2;
OX	RX MEDLINE=99065613; PubMed=9951916;	RX MEDLINE=99065613; PubMed=9951916;
RA	SEQUENCE FROM N.A.	RA None;
RA	MEDLINE=20195006; PubMed=10731132;	RT "Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology." The C. elegans Sequencing Consortium. ; RT science 282:2012-2018(1998).
RA	ADAMS M.D., CELENIK S.E., HOLT R.A., EVANS C.A., GOCAYNE J.D., AMANATIDES P.G., SCHERER S.E., LI P.W., HOSKINS R.A., GALLE R.F., GEORGE R.A., LEWIS S.E., RICHARDS S., ASHBURNER M., HENDERSON S.N., SUTTON D.J.R., YANDELL M.D., ZHANG Q., CHEN L.X., BRANDON R.G.C., ROGERS Y.-H.G., BLAZEJ R.G., CHAMPION M., PFLIFFER B.D., WAN K.H., DOYLE C., BAXTER E.G., HEIT G., NELSON C.R., MIKLOS G.L.G., ABRIJ J.F., AGBALA A.I., AN H.-J., ANDREWS PIASTROK C., BALDWIN D., BAILEY R.M., BASU A., BAXENDALE J., BAYRAKTAROGLU L., BEASLEY B.M., BEESON K.Y., BENOS P.V., BERNAN B.P., BHANDARI D., BOLSNAKOV S., BORKOVIC D., BOUCH D., BOUC K.J., BROOKSTEIN P., BROTTLER P., BURTIS K.C., BUSAM D.A., BUTLER H., CADIEU E., CENTER A., CHANDRA I., CHERRY J.M., CAWLEY S., DALILKE C., DAVENPORT L.B., DAVIES P., DE PABLOS B., DELCHER A., DENG A., DENG J., DIELTZ S.M., DODSON K.R., DOUP L.E., DOWNES M., DUGAN-ROCHA S., DUNKOV B.C., DUNN P., DURBIN K.J., EVANGELISTA C., FERRARI S., FLEISCHMANN W., FOSLER C., GARG N.S., GELBART W.M., GLASSER K., GLODEK A., GORELL J.H., GU Z., GUAN P., HARRIS M., HARRIS N.L., HARVEY D., HEMAN T.J., HERNANDEZ J.R., HOUCK J., HOSTIN D., HOUSTON K.A., HOWLAND T.J., WEI M.-H., TIBEGWAN C., JALILI M., KALUSH F., KARPEN G.H., KE Z., KENNISON J.A., KETCHUM K.A., KIMMEL B.E., KODIVA C.D., KRAFT S., KRAVITZ S., KULP D., LAI Z., LASKO P., LEI Y., LEVITSKY A.A., LI J., LI Z., LIANG Y., LIN X., LIU X., MATTEE B., MCINTOSH T.C., MCLEOD M.P., MCPHARSON D., MERKULOV G., MILASHINA N.V., MOBARRY C., MORRIS J., MOSHTRAFI A., MOUNT S.M., MUZYK N., MURPHY B., MUZNY D.M., NELSON D.L., NELSON D.R., NELSON K.A., NIXON K., NUSSKERN D.R., PACLEB J.M., PALIZZOTTO M., PITTMAN G.S., PAUND S., PURI V., REESE M.G., REINERT K., REMINGTON K., SAUNDERS R.D.C., SCHHEELER F., SHEN H., SHUE B.C., SIDEN-KIAMOS I., SIMPSON M., SKUPSKI M.P., SMITH T., SPIER E., SPRADING A.C., STAPLETON M., STRONG R., SUN E., SWIRSKA S., TECTOR C., TURNER R., VENTER E., WANG A.H., WANG X., WANG Z.Y., WASBARMAN D.A., WORRELL G.M., WEISSENBACH J., WILLIAMS S.M., WOODAGE T., YEH R.-F., ZAVIERI J.S., ZHAN M., YAO Q.A., YE J., ZHENG F.N., ZHONG W., ZHOU X., ZHU S., ZHU X., ZHENG L., ZHENG X.H., ZHONG F.N., ZHONG W., ZHOU X., ZHU S., ZHU X., SMITH H.O., GIBBS R.A., MYERS B.W., RUBIN G.M., VENTER J.C., "The genome sequence of <i>Drosophila melanogaster</i> ," RT	
RA	Q9GR8 PRELIMINARY; PRT; 298 AA.	Q9GR8 PRELIMINARY; PRT; 298 AA.
ID	AC Q9GR8; 18, Created)	AC Q9GR8; 18, Created)
AC	DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)	DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT	DT 01-OCT-2001 (TREMBLrel. 19, Last annotation update)	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN	PREDICTED NUCLEOTIDYLTRANSFERASE CAS2298.	GN

OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 RN [1] NCBI_TaxID:1488;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VRM B-1787;
 RX MEDLINE=21359325; PubMed=1466286;
 RX Noellings J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J.J., Wolf Y.I.,
 Tatusev R.I., Sabathe F., Doucette L., Soucaille P., Daly M.J.,
 Bennett G.N., Konon E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL; AE007730; AAK80254 1; -.
 DR InterPro; IPR005934; NTP Transe.
 DR Pfam; PF010109; NTP trans_E_2_1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 298 AA; 35000 MW;
 9986B0A8FEED303 CRC64;
 Query Match 38.8%; Score 47; DB 16; Length 298;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 LARYLNSQAYSAYY 21
 Db Db 142 LCKYIINKRYTYY 157

RESULT 13
 OS8IAY2 PRELIMINARY; PRT; 758 AA.
 JD Q8IAY2 PRELIMINARY; PRT; 758 AA.
 AC Q8IAY2; 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN MALP_88.
 CS Plasmidium falciparum (isolate 3D7).
 OC Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN [1] NCBI_TaxID:36322;
 RP SEQUENCE FROM N.A.
 FA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 Quail M., Barrell B.,
 RL Submitted (SEP-2002) to the ENSEMBL/GenBank/DDBJ databases.
 DR AL844507; CAD51228.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 758 AA; 90296 MW;
 B9C395E9D9103492 CRC64;
 Query Match 38.8%; Score 47; DB 5; Length 758;
 Best Local Similarity 69.2%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 RCYLSNSQAYSAY 20
 Db Db 121 RCYLNSNLYSKX 133

RESULT 14
 Q8IM09 PRELIMINARY; PRT; 7149 AA.
 AC Q8IM09; 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PF14_0084.
 CS Plasmidium falciparum (isolate 3D7).
 OC Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=D7;
 RX Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 Nelson K.E., Bowman S., Paulsen I.T., James K.,
 Carlton J.M., Pain A., Salzberg S.L., Craig A., Kyes S.,
 Eisen J.A., Rutherford K., Suh B., Peterson J., Angiuoli S.,
 Chan M.-S., Nene V., Shallom S.J., Suh B., Peterkin J., Vaidya A.B.,
 Pertea M., Allen J., Hatt D., Mather M.W., Roos D.S., Ralph S.A.,
 Martin D.M.A., Fairlamb A.H., Braunholz M.J., Roos D.S.,
 McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 Verter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 Fraser C.M., Barrell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum.";
 RT Nature 419:998-511(2002).
 RL EMBL; AE014817; AAN36596.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 7149 AA; 847876 MW;
 Query Match 38.4%; Score 46.5; DB 5;
 Best Local Similarity 38.1%; Pred. No. 6.4e+02;
 Matches 8; Conservative 6; Mismatches 4; Indels 3; Gaps 1;
 Qy 2 NLQLLARCYLSNSQAYSAYI 22
 Db 2496 NVRL---CYNNNSSEGYSKYHV 2513

RESULT 15
 OS8958 PRELIMINARY; PRT;
 ID OS8958; 07, Created)
 AC OS8958;
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 0, Last annotation update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein PH1225.
 GN PH1225.
 OS Pyrococcus horikoshii.
 OC Archaea; Eurarchaeota; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OC Pyrococcus.
 RN [1] NCBI_TaxID:51953;
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayasi Y., Sawada M., Horikawa H., Hino Y., Hino Y., Nagai Y.,
 Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 Sakai M., Ogura K., Otsuka R., Ohfuku Y.,
 Furukoshi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
 Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Matsuchi Y., Shizuya H., Kiuchi H.,
 RA Mauchii Y.,
 RT Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeabacterium, Pyrococcus horikoshii OT3.",
 RT DNA Res. 5:55-76 (1998).
 DR AP00005; BAA30325.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 173 AA; 19986 MW; 7D7FD7D9BB798B1B CRC64;

Query Match 38.0%; Score 46; DB 17; Length 173;
 Best Local Similarity 45.8%; Pred. No. 15;
 Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 VNLLQLLARCYLSNSQAYSAYIK 24
 Db 62 VGIVLWAICYFOVSKAYGKLK 85

Search completed: February 2, 2004, 12:50:22
 Job time : 180 secs

ALIGNMENTS

RESULT 1
US-1036-492-14
Sequence 14, Application US/10036492
; Publication No. US20020164757A1
GENERAL INFORMATION:
; APPLICANT: HEMERYL, ADRIANA
; APPLICANT: FERREIRA, PAULO
; APPLICANT: ROMBAUTS, STEPHANE
; TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted.

33

Result No.	Score	%	Query Match	Length	DB	ID	Description
SOURCE1							

Alignment Scores: **Score 10** **Score 10**

Score: 121.00 Matches: 24 ; LENGTH: 2512
 Percent Similarity: 100.00% Conservative: 0 ; TYPE: DNA
 Best Local Similarity: 100.00% Mismatches: 0 ; ORGANISM: Arabidopsis thaliana
 Query Match: 100.00% Indels: 0 ; US-10-036-492-27
 DB: 14 Gaps: 0

US-10-036-492-6 (1-24) × US-10-036-492-14 (1-2401)

Qy 1 ValAsnLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 109 GTGAACTCTGCAATTGTAGCCAGGTACTTGAGTAACGTCAAGCTATACTGCAAT 168

Qy 21 TyrIleLeuLys 24
 Db 169 TATATCCCTAAA 180

RESULT 2
 US-10-036-492-9
 Sequence 9, Application US/10036492
 Publication No. US20020164757A1

GENERAL INFORMATION
 APPLICANT: HEMERY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE

TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 211943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 9
 LENGTH: 2434
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana

US-10-036-492-9

Alignment Scores:
 Pred. No.: 6.37e-10 Length: 2434 ; SEQ ID NO 15
 Score: 121.00 Matches: 24 ; LENGTH: 2220
 Percent Similarity: 100.00% Conservative: 0 ; TYPE: DNA
 Best Local Similarity: 100.00% Mismatches: 0 ; ORGANISM: Arabidopsis thaliana
 Query Match: 100.00% Indels: 0 ; US-10-036-492-15
 DB: 14 Gaps: 0

US-10-036-492-6 (1-24) × US-10-036-492-9 (1-2434)

Qy 1 ValAsnLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 109 GTGAACTCTGCAATTGTAGCCAGGTACTTGAGTAACGTCAAGCTATACTGCAAT 168

Qy 21 TyrIleLeuLys 24
 Db 169 TATATCCCTAAA 180

RESULT 3
 US-10-036-492-27/c
 Sequence 27, Application US/10036492
 Publication No. US20020164757A1

GENERAL INFORMATION
 APPLICANT: HEMERY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE

TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 211943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27

Alignment Scores:
 Pred. No.: 6.64e-10 Length: 2512
 Score: 121.00 Matches: 24 ; LENGTH: 2220
 Percent Similarity: 100.00% Conservative: 0 ; TYPE: DNA
 Best Local Similarity: 100.00% Mismatches: 0 ; ORGANISM: Arabidopsis thaliana
 Query Match: 100.00% Indels: 0 ; US-10-036-492-15
 DB: 14 Gaps: 0

US-10-036-492-6 (1-24) × US-10-036-492-27 (1-2512)

Qy 1 ValAsnLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 2326 GTGAACTCTGCAATTGTAGCCAGGTACTTGAGTAACGTCAAGCTATACTGCAAT 2267

Qy 21 TyrIleLeuLys 24
 Db 2266 TATATCCCTAAA 2255

RESULT 4
 US-10-036-492-15
 Sequence 15, Application US/10036492
 Publication No. US20020164757A1
 GENERAL INFORMATION:
 APPLICANT: HEMERY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE
 TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 211943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 15

Alignment Scores:
 Pred. No.: 5.56e-05 Length: 2220
 Score: 91.00 Matches: 18 ; LENGTH: 2220
 Percent Similarity: 87.00% Conservative: 3 ; TYPE: DNA
 Best Local Similarity: 75.00% Mismatches: 3 ; ORGANISM: Arabidopsis thaliana
 Query Match: 75.21% Indels: 0 ; US-10-036-492-15
 DB: 14 Gaps: 0

US-10-036-492-6 (1-24) × US-10-036-492-15 (1-2220)

Qy 1 ValAsnLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 106 GTTAAATTGCAGCTATTGCCACAGCTACCTGAGATAATCAAAGTTACAGTCAT 165

Qy 21 TyrIleLeuLys 24
 Db 166 CATCTGCTANAG 177

RESULT 5
 US-09-918-995-17374
 Sequence 17374, Application US/0991895
 Publication No. US20030071623A1
 GENERAL INFORMATION:
 APPLICANT: HYSEG, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30
; PRIORITY APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO: 17374
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-17374

Alignment Scores:
Pred. No.: 0.616 Length: 419
Score: 61.00 Matches: 12
Percent Similarity: 68.18% Conservative: 3
Best Local Similarity: 54.55% Mismatches: 7
Query Match: 50.41% Indexes: 0
DB: 11 Gaps: 0

US-10-036-492-6 (1-24) × US-09-918-995-17374 (1-419)

Qy 3 LeuGlnLeuAlaArgCystYleLeuSerAsnSerGlnAlaTyrSerAlaTyrTyrile 22
Db 201 TTGCCTTACTGGCACCTTATTACCGTCAGGGCATATAAGCATAGATC 260

Qy 23 LeuIys 24
Db 261 TTGAAA 266

RESULT 6
US-10-027-632-101808
; Sequence 101808, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/198,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,576
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO: 101808
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101809

Alignment Scores:
Pred. No.: 124 Length: 2318
Score: 53.00 Matches: 9
Percent Similarity: 68.18% Conservative: 6
Best Local Similarity: 40.91% Mismatches: 7
Query Match: 43.80% Indexes: 0
DB: 13 Gaps: 0

US-10-036-492-6 (1-24) × US-10-027-632-101809 (1-2318)

Qy 2 AsnLeuGlnLeuAlaArgCystYleLeuSerAsnSerGlnAlaTyrSerAlaTyrTyr 21
Db 690 AATATGAAATTTGACTCTGCTCTAACACTCTGGATGAAAAATCTATT 749

Qy 22 IleLeu 23
Db 750 TRACTT 755

RESULT 8
US-10-027-632-101808
; Sequence 101808, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO: 101808
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101808

Alignment Scores:
Pred. No.: 124 Length: 2318
Score: 53.00 Matches: 9
Percent Similarity: 68.18% Conservative: 6
Best Local Similarity: 43.80% Mismatches: 7
Query Match: 43.80% Indexes: 0
DB: 13 Gaps: 0

US-10-036-492-6 (1-24) × US-10-027-632-101808 (1-2318)

Qy 2 AsnLeuGlnLeuAlaArgCystYleLeuSerAsnSerGlnAlaTyrSerAlaTyrTyr 21

PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: US 60/185,218
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: US 60/167,363
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: US 60/156,358
 PRIOR FILING DATE: 1999-09-28
 PRIOR APPLICATION NUMBER: US 60/146,002
 PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 325720
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 101808
 LENGTH: 2318
 TYPE: DNA
 ORGANISM: Human
 US-10-027-632-101808

Alignment Scores:
 Pred. No.: 124 Length: 2318
 Score: 53.00 Matches: 9
 Percent Similarity: 68.18% Conservative: 6
 Best Local Similarity: 40.91% Mismatches: 7
 Query Match: 43.80% Indels: 0
 DB: 14 Gaps: 0

RESULT 10
 US-10-114-170-14
 ; Sequence 14, Application US/10114170
 ; Publication No. US20030023075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; BURLAND, Valerie
 ; Perna, Nicole T.
 ; Plunkett, Guy
 ; Welch, Rod
 TITLE OF INVENTION: No. US20030023075A1 Sequences of E. coli O157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/114,170
 FILING DATE: 01-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/453,702
 FILING DATE: 03-Dec-1999
 APPLICATION NUMBER: 60/110,955
 FILING DATE: 04-Dec-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 PREFERRED DOCUMENT NUMBER: 960296.95017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12886
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-10-114-170-14

Alignment Scores:
 Pred. No.: 1.17e+03 Length: 12886
 Score: 53.00 Matches: 10
 Percent Similarity: 64.29% Conservative: 8
 Best Local Similarity: 35.71% Mismatches: 6
 Query Match: 43.80% Indels: 4
 DB: 15 Gaps: 1

RESULT 11
 US-10-036-492-6 (1-24) x US-10-114-170-14 (1-12886)
 Qy 1 ValAsnLeuGlnLeuLeuSerAsnSerGlnAla 16

Alignment Scores:
 Pred. No.: 124 Length: 2318
 Score: 53.00 Matches: 9
 Percent Similarity: 68.18% Conservative: 6
 Best Local Similarity: 40.91% Mismatches: 7
 Query Match: 43.80% Indels: 0

Db 9431 GATATCGAGTAATACGTAATGGCAATTCTTAAAGCCGTCAGTT 9490
 QY 17 TyrSerAlaTyryileuLys 24
 Db 9491 AAGATGCTTTCACCTGGTGA 9514

RESULT 11
 US-10-027-632-199214
 ; Sequence 199214, Application US/10027632
 ; Publication No. US20030204075A9

; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827-129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/238,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-09-11
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325/20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 199214
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-199214

Alignment Scores:
 Pred. No.: 30 Length: 585
 Score: 52.00 Matches: 11
 Percent Similarity: 68.42% Conservative: 2
 Best Local Similarity: 57.89% Mismatches: 2
 Query Match: 42.98% Indexes: 4
 DB: 13 Gaps: 1

US-10-036-492-6 (1-24) × US-10-027-632-199215 (1-585)
 QY 8 ArgCystTyrlleuSerAsn-----SerGlnAlaTyryileuSerAsn-----
 Db 166 AAATGTTATTATCAATGCTTACACATCAAACCTTCTGCATATTATA 222

RESULT 12
 US-10-027-632-199215
 ; Sequence 199215, Application US/10027632
 ; Publication No. US20030204075A9

; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827-129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-01-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325/20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 199214
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-199214

Alignment Scores:
 Pred. No.: 30 Length: 585
 Score: 52.00 Matches: 11
 Percent Similarity: 68.42% Conservative: 2
 Best Local Similarity: 57.89% Mismatches: 2
 Query Match: 42.98% Indexes: 4
 DB: 14 Gaps: 1

US-10-036-492-6 (1-24) × US-10-027-632-199214 (1-585)
 QY 8 ArgCystTyrlleuSerAsn-----SerGlnAlaTyryileuSerAsn-----
 Db 166 AAATGTTATTATCAATGCTTACACATCAAACCTTCTGCATATTATA 222

```

RESULT 14
US-10-027-632-199215
Sequence 199215, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198, 006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185, 218
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 60/167, 363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156, 358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146, 002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO: 199215
SEQUENCE: FastSEQ for Windows Version 4.0
LENGTH: 585
TYPE: DNA
ORGANISM: Human
US-10-027-632-199215

Alignment Scores:
Pred. No.: 30 Length: 585
Score: 52.00 Matches: 11
Percent Similarity: 68.42% Conservative: 2
Best Local Similarity: 57.89% Mismatches: 4
Query Match: 42.98% Indels: 4
DB: 14 Gaps: 1

US-10-036-492-6 (1-24) x US-10-027-632-26594 (1-722)

Qy 8 ArgCystYLeuSerAn-----SerGinAlaTyrSerAlaTyrTyrIle 22
Db 166 AAATGTTATTCAATGGCTACAAACATAAACCTATTTCTGCATATTATA 222

RESULT 15
US-10-027-632-26594
Sequence 26594, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 10/027, 632
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 006
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198, 476
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167, 363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156, 358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146, 002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720

```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 2, 2004, 13:26:34 ; Search time 163 Seconds

(without alignments)

64.989 Million cell updates/sec

Title: US-10-036-492-6

Perfect score: 121

Sequence: 1 VNLLQLLARYLNSQNSAYYVLLK 24

Scoring table: BL0SUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=x1h

-Q=cgn2_1/uspto.spoof10S10C6492/runat02022004_085034_13476/app_query.fasta_1.199

-DB=ISSUED_PATENTS_NA -QFORMAT=fasta -SUFFIX=nni -MINNAME=0 -MAXNAME=62 -TRANS=human0 -CDI=0

-LOOPEXT=-UNITS-BITS -START=-1 -END=-1 -NORM=ext -THR=MAX=100 -THR_MIN=0 -ALIGN=N15

-LIST=45 -DOCALLIGN=200 -LOCAL -SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=N15

-MODE=0 -NORM=ext -HEAPSIZE=500 -MAXLEN=2000000000

-USER=US-0033492 @cgn_1.1_56 @runat02022004_085034_13476 -NCPU=6 -ICPU=3

-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG

-DEV TIMEOUT=30 -WARN -TIMEOUT=30 -XGAP0=10 -XGAPEXT=0.5 -FGAP0=6

-FGAPEXT=7 -YGAPO=10 -YGAPEXT=0.5 -DEL0P=6 -DELEXT=7

Database : Issued_Patents_NA.*

1: /cgn2_6/podata/1/inav5A_COMB.seq:*

2: /cgn2_6/podata/1/inav5B_COMB.seq:*

3: /cgn2_6/podata/1/inav7A_COMB.seq:*

4: /cgn2_6/podata/1/inav7B_COMB.seq:*

5: /cgn2_6/podata/1/inapctus_COMB.seq:*

6: /cgn2_6/podata/1/inav/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	59	2472	1	US-08-425-299A-2	Sequence 2, Appli	Sequence 2460, AP
c 2	53	43.8	4011	4	US-09-134-001C-2460	Sequence 14, Appli
c 3	53	43.8	12886	4	US-09-453-702B-14	Sequence 2936, AP
c 4	49	40.5	1098	4	US-09-107-532A-2936	Sequence 812, AP
c 5	48	39.7	897	4	US-09-328-352-B12	Sequence 8, Appli
c 6	48	39.7	2999	2	US-09-014-969-B8	Sequence 3, Appli
c 7	48	39.7	90541	4	US-09-759-359A-3	Sequence 4, Appli
c 8	47	38.8	1308	4	US-09-526-993-4	Sequence 3, Appli
c 9	47	38.8	2167	4	US-09-526-993-3	Sequence 1, Appli
c 10	47	38.8	2636	1	US-08-253-785-1	Sequence 2, Appli
c 11	47	38.8	3224	4	US-09-526-993-2	Sequence 1, Appli
c 12	47	38.8	6070	4	US-09-526-993-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
 US-08-425-299A-2
 Sequence 2, Application US/08425299A
 / Patent No. 5726025
 GENERAL INFORMATION:
 / APPLICANT: Kirschner, Marc W.
 / APPLICANT: King, Randall W.
 / APPLICANT: Peters, Jean-Michael
 / TITLE OF INVENTION: Assay and Reagents for Detecting Inhibitors
 / TITLE OF INVENTION: of Ubiquitin Dependent Degradation of
 / TITLE OF INVENTION: Cell Cycle Regulatory Proteins
 / NUMBER OF SEQUENCES: 14
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: LAHIVE E. COCKFIELD
 / STREET: 60 State Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: ASCII (text)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/425-299A
 / FILING DATE: 20-APR-1995
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Vincent, Matthew P.
 / REGISTRATION NUMBER: 36,709
 / REFERENCE/DOCKET NUMBER: HNI-014
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (617) 227-7400
 / TELEFAX: (617) 227-5941
 / INFORMATION FOR SEQ ID NO: 2:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 2472 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2469
US-08-425-299A-2

Alignment Scores:
Pred. No.: 2.71 Length: 2472
Score: 59.0 Matches: 12
Percent Similarity: 68.18% Conservative: 3
Best Local Similarity: 54.55% Mismatches: 7
Query Match: 48.66% Indels: 0
DB: 1 Gaps: 0

US-10-036-492-6 (1-24) x US-08-425-299A-2 (1-2472)

Qy      3 LeuGlnIleuLeuAlaArgCysteYLeuSerAsnSerGlnAlaTyrSerAlaTyrIle 22
Db      121 TGTGTTTACTGGAACTGTATACCGCTCAAGGAAGGCATATAAGCATATAAGCTAC 180

Qy      23 LeuLys 24
Db      181 TIGAAA 186

RESULT 2
US-09-134-001C-2460/c
Sequence 2460, Application US/09134001C
Patent No. 63280370
GENERAL INFORMATION:
APPLICANT: Lyman Doucette-Stamm et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTG-C-007
CURRENT APPLICATION NUMBER: US/09-134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2460
LENGTH: 1011
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2460

Alignment Scores:
Pred. No.: 8.72 Length: 1011
Score: 53.0 Matches: 11
Percent Similarity: 69.57% Conservative: 5
Best Local Similarity: 47.83% Mismatches: 7
Query Match: 43.80% Indels: 0
DB: 4 Gaps: 0

US-10-036-492-6 (1-24) x US-09-134-001C-2460 (1-1011)

Qy      1 ValAsnIleuGlnIleuLeuAlaArgCysteYLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
Db      913 GTAGGACTGTGCTTACTGCATGTCACCTAACGTTGAGCAATCTATAAACCAAAT 854

Qy      21 TyrIleLeu 23
Db      853 TACCTGCCT 845

RESULT 3
US-09-453-702B-14
Sequence 14, Application US/09453702B
Patent No. 6365723

```


US-10-036-492-6 (1-24) X US-09-014-969-8 (1-2999)

Qy 1 ValAsnLeuGlnLeuLeuAlaArgCystYleSerAsn----- 13

Db 2695 GTCATCGCAATGTCACACATGTACACTGTAATTCTGACAAATTAAATGTT 2636

Qy 14 -----SerGlnAlaTyrSerAlaTyrTyrIleLeu 23

Db 2635 ACTAGAGATAACAGATAAACATTCTACTATTTA 2597

RESULT 7

US-09-759-359A-3

; Sequence 3, Application US/09759359A

; Patent No. 6492153

; GENERAL INFORMATION:

; APPLICANT: ABU-THREDEH, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACIDS ENCODING HUMAN KINASE PROTEINS, AND USES ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CLO001043

; CURRENT APPLICATION NUMBER: US/09/759,359A

; CURRENT FILING DATE: 2001-01-16

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 90541

; TYPE: DNA

; ORGANISM: Human

US-09-759-359A-3

Alignment Scores:

Pred. No.:	1.34e+04	Length:	90541
Score:	48.10	Matches:	7
Percent Similarity:	87.50%	Conservative:	7
Best Local Similarity:	43.75%	Mismatches:	2
Query Match:	39.67%	Indels:	0
DB:	4	Gaps:	0

US-10-036-492-6 (1-24) X US-09-759-359A-3 (1-90541)

Qy 9 CystYleSerAsnSerGlnAlaTyrSerAlaTyrTyrIleLeu 24

Db 73862 TGTTCCTGGCCATTAGCAGCTTCTAGTGGTTTACTTAGG 73909

RESULT 8

US-09-526-993-4/C

; Sequence 4, Application US/09526993

; Patent No. 6465715

; GENERAL INFORMATION:

; APPLICANT: Zwaal, Richard

; APPLICANT: Roelens, Ingele

; APPLICANT: Bogart, Thierry

; TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS

; FILE REFERENCE: B0192/7012/ERG/KA

; CURRENT APPLICATION NUMBER: US/09/526,993

; CURRENT FILING DATE: 2000-03-16

; EARLIER APPLICATION NUMBER: U.K. 9906018.8

; EARLIER FILING DATE: 1999-03-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 1308

; TYPE: DNA

; ORGANISM: Caenorhabditis Elegans

US-09-526-993-4

Alignment Scores:

Pred. No.:	114	Length:	1308
Score:	47.00	Matches:	11
Percent Similarity:	58.33%	Conservative:	3
Best Local Similarity:	45.83%	Mismatches:	10
Query Match:	38.84%	Indels:	0
DB:	4	Gaps:	0

US-10-036-492-6 (1-24) X US-09-526-993-3 (1-2167)

Qy 1 ValAsnLeuGlnLeuLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20

Db 356 ATAAACTTATTATTCAACATGATTAAATAAATTAATCGCTTTCAGCGTT 297

RESULT 9

US-09-526-993-3/C

; Sequence 3, Application US/09526993

; Patent No. 6465715

; GENERAL INFORMATION:

; APPLICANT: Zwaal, Richard

; APPLICANT: Asaert, Wouter

; APPLICANT: Roelens, Ingele

; APPLICANT: Bogart, Thierry

; TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS

; FILE REFERENCE: B0192/7012/ERG/KA

; CURRENT APPLICATION NUMBER: US/09/526,993

; CURRENT FILING DATE: 2000-03-16

; EARLIER APPLICATION NUMBER: U.K. 9906018.8

; EARLIER FILING DATE: 1999-03-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2167

; TYPE: DNA

; ORGANISM: Caenorhabditis Elegans

US-09-526-993-3

Alignment Scores:

Pred. No.:	210	Length:	2167
Score:	47.00	Matches:	11
Percent Similarity:	58.33%	Conservative:	3
Best Local Similarity:	45.83%	Mismatches:	10
Query Match:	38.84%	Indels:	0
DB:	4	Gaps:	0

US-10-036-492-6 (1-24) X US-09-526-993-3 (1-2167)

Qy 1 ValAsnLeuGlnLeuLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20

Db 356 ATAAACTTATTATTCAACATGATTAAATAAATTAATCGCTTTCAGCGTT 297

RESULT 10

US-08-253-785-1/C

; Sequence 1, Application US/08253785

; Patent No. 5633253

; GENERAL INFORMATION:

; APPLICANT: Colbert, James T.

; APPLICANT: Held, Bruce M.

; APPLICANT: Wurtele, Eve S.

; APPLICANT: Dietrich, Paul S.

; TITLE OF INVENTION: ROOT PREFERENTIAL PROMOTER

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Sandoz Agro, Inc.

; STREET: 975 California Avenue

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM: -

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.1., Version #1.25
 CURRENT APPLICATION NUMBER: US/08/253,785
 FILING DATE:
 CLASIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Marcus-Wynne, Lynn
 REGISTRATION NUMBER: 34,869
 REFERENCE/DOCKET NUMBER: 135-1089
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/857-3588
 TELEFAX: 415/857-1125
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2636 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQ ID NO: 1

Alignment Scores:
 Pred. No.: 266 Length: 2636
 Score: 47.00 Matches: 8
 Percent Similarity: 57.89% Conservative: 3
 Best Local Similarity: 42.11% Mismatches: 8
 Query Match: 1.84% Indels: 0
 DB: 1 Gaps: 0

US-10-036-492-6 (1-24) x US-08-253-785-1 (1-2636)

Qy 5 LeuLeuAlaLargCystTrieLeuSerAsnSerGlnAlaTyrSerAlaTyrTyrIleu 23
 Db 564 CTTTTGCCAGTGTTACACTGACAAGTACACATTTCATTATGGCTT 508

RESULT 11
 US-09-526-993-2/c
 Sequence 2, Application US/09526993
 Patent No. 6465715
 GENERAL INFORMATION:
 APPLICANT: Zwaal, Richard
 APPLICANT: Aaert, Wouter
 APPLICANT: Roelens, Ingele
 APPLICANT: Bogaert, Thierry
 TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS
 FILE REFERENCE: 20192/7012.ERG/KA
 CURRENT APPLICATION NUMBER: US/09/526,993
 CURRENT FILING DATE: 2000-03-16
 EARLIER APPLICATION NUMBER: U.K. 9906018.8
 EARLIER FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 2

TYPE: DNA
 ORGANISM: Caenorhabditis Elegans

Alignment Scores:
 Pred. No.: 340 Length: 3224
 Score: 47.00 Matches: 11
 Percent Similarity: 58.33% Conservative: 3
 Best Local Similarity: 45.83% Mismatches: 10
 Query Match: 1.84% Indels: 0
 DB: 4 Gaps: 0

US-10-036-492-6 (1-24) x US-09-526-993-2 (1-3224)

Qy 1 ValAsnLeuGlnLeuLeuAlaLargCystTrieLeuSerAsnSerGlnAlaTyrTyrIleu 20
 Db 1413 ATAAACTTATTATTGACATGATTAAATTAAATCGCTTTCAGCCTT 1354

Qy 21 TyrIleLeuLys 24
 Db 1353 TTAACTTAAA 1342

RESULT 12
 US-09-526-993-1/c
 Sequence 1, Application US/09526993
 Patent No. 6465715
 GENERAL INFORMATION:
 APPLICANT: Zwaal, Richard
 APPLICANT: Aaert, Wouter
 APPLICANT: Roelens, Ingele
 APPLICANT: Bogaert, Thierry
 TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS
 FILE REFERENCE: 20192/7012.ERG/KA
 CURRENT APPLICATION NUMBER: US/09/526,993
 CURRENT FILING DATE: 2000-03-16
 EARLIER APPLICATION NUMBER: U.K. 9906018.8
 EARLIER FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 1

TYPE: DNA
 ORGANISM: Caenorhabditis Elegans

Alignment Scores:
 Pred. No.: 735 Length: 6070
 Score: 47.00 Matches: 11
 Percent Similarity: 58.33% Conservative: 3
 Best Local Similarity: 45.83% Mismatches: 10
 Query Match: 1.84% Indels: 0
 DB: 4 Gaps: 0

US-10-036-492-6 (1-24) x US-09-526-993-1 (1-6070)

Qy 1 ValAsnLeuGlnLeuLeuAlaLargCystTrieLeuSerAsnSerGlnAlaTyrTyrIleu 20
 Db 4259 ATAACATTATTATTATTGAACTGAGTACACATTTCATTATGGCTTTACGCGTT 4200

Qy 21 TyrIleLeuLys 24
 Db 4199 TTAACTTAAA 4188

RESULT 13
 US-09-526-993-10/c
 Sequence 10, Application US/09526993
 Patent No. 6465715
 GENERAL INFORMATION:
 APPLICANT: Zwaal, Richard
 APPLICANT: Aaert, Wouter
 APPLICANT: Roelens, Ingele
 APPLICANT: Bogaert, Thierry
 TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS
 FILE REFERENCE: 20192/7012.ERG/KA
 CURRENT APPLICATION NUMBER: US/09/526,993
 CURRENT FILING DATE: 2000-03-16
 EARLIER APPLICATION NUMBER: U.K. 9906018.8
 EARLIER FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 10

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: plasmid pGF2013

Alignment Scores:
 Pred. No.: 747 Length: 6157
 Score: 47.00 Matches: 11
 Percent Similarity: 58.33% Conservative: 3
 Best Local Similarity: 45.83% Mismatches: 10
 Query Match: 1.84% Indels: 0
 DB: 4 Gaps: 0

US-09-526-993-10

Score: 47.00 Matches: 11
 Percent Similarity: 58.33% Conservative: 3
 Best Local Similarity: 45.83% Mismatches: 10
 Query Match: 38.84% Indels: 0
 DB: 4 Gaps: 0

US-10-036-492-6 (1-24) x US-09-526-993-10 (1-6157)

Qy 1 ValAsnLeuGlnIleLeuAlaArgCysteLeuSerAnSerGlnAlaTyrSerAlaTyr 20
 Db 2446 ATAACTATTATTTATTGGAAACGATGATTAAATAATTAAATCGTTTCAGGTT 2387

Qy 21 TyrIleLeuLys 24
 Db 2386 TTAATTAAAAA 2375

RESULT 14

US-09-526-993-8/c
 Sequence 8, Application US/09526993
 Patent No. 6465715
 GENERAL INFORMATION:
 APPLICANT: Zwaal, Richard
 APPLICANT: Asaert, Wouter
 APPLICANT: Roelens, Ingele
 APPLICANT: Bogaert, Thierry
 TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C. ELEGANS
 FILE REFERENCE: B09/2012/ERC/KA
 CURRENT APPLICATION NUMBER: US/09/526,993
 CURRENT FILING DATE: 2000-03-16
 EARLIER APPLICATION NUMBER: U.K. 9906018.8
 EARLIER FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 8
 LENGTH: 6202
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Plasmid pgf2006

US-09-526-993-8

Alignment Scores:
 Pred No.: 754 Length: 6202
 Score: 47.00 Matches: 11
 Percent Similarity: 58.13% Conservative: 3
 Best Local Similarity: 45.83% Mismatches: 10
 Query Match: 38.94% Indels: 0
 DB: 4 Gaps: 0

US-10-036-492-6 (1-24) x US-09-526-993-8 (1-6202)

Qy 1 ValAsnLeuGlnIleLeuAlaArgCysteLeuSerAnSerGlnAlaTyrSerAlaTyr 20
 Db 361 ATAACTATTATTTATTGGAAACGATGATTAAATAATTAAATCGTTTCAGGTT 302

Qy 21 TyrIleLeuLys 24
 Db 301 TTAATTAAAAA 290

RESULT 15

US-09-134-001C-2523
 Sequence 2523, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: TC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame plus p2n model

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Run on: February 2, 2004, 13:02:44 ; Search time 1605 Seconds
          (without alignments)
          40.365 Million cell updates/sec

Title: US-10-036-492-6

Perfect score: 121
Sequence: 1 VNIQLLARCYLSNSQAYSAYTILK 24

Scoring table: BLOSUM62
Xgapext 0.5
Ygapext 0.5
Fgapext 0.5
Dgapext 0.5
Delett 7.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing First 45 summaries
```

Command line parameters:

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-MCDE=frame+DBN.model -DEV=x1h
-Q=/USP01/USP01.spool -DB=N GeTeSeq_19Jun03 -QMTM=fastap -SUFIX=TGT -MINWTCH=0.1 -LOCFL=0
-LOCPXT=0 -UNITS=bits -START=1 -END=1 -BITS=1 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=100 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFORMAT=PELTO -NORMALIZE=1 -HEAISIZEMAXLEN=0 -MINLEN=0 -MAXLEN=20000000000
-USBR=USI0336432 @CCN 1_1_312 @runat 02020204 085033 -CPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=0 -TIMEOUT=30 -WARN TIMEOUT=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=10 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7
```

Database :

```
N_GeTeSeq_19Jun03 : *
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
1	121	100.0	2401	22	AAP56506	
2	121	100.0	2434	22	AAP56505	
3	91	75.2	486	24	ABK93343	
4	91	75.2	498	24	ABK93344	
5	91	75.2	1557	24	ABK93357	
6	91	75.2	2116	24	ABK93356	
7	91	75.2	2220	22	AAP56507	
8	91	75.2	2235	24	ABK93342	
9	91	75.2	2235	24	ABK93352	
10	91	75.2	2235	24	ABK93354	
11	91	75.2	2235	24	ABK93354	
12	91	75.2	2313	24	ABK93358	
13	91	75.2	2316	21	AAC50257	
14	91	75.2	2480	24	ABK93341	
15	91	75.2	4577	24	ABK93340	
16	91	75.2	4577	24	ABK93345	
17	91	75.2	4577	24	ABK93346	
18	91	75.2	4577	24	ABK93347	
19	91	75.2	4577	24	ABK93348	
20	91	75.2	4577	24	ABK93349	
21	91	75.2	4577	24	ABK93350	
22	91	75.2	4577	24	ABK93351	
23	91	75.2	4577	24	ABK93352	
24	59	48.8	314	21	AAC01810	
25	59	48.8	406	14	AQ095610	
26	59	48.8	2477	17	AAT41774	
27	59	48.8	2747	23	AAS46782	
28	59	48.8	3320	16	AQ091200	
C	29	53	43.8	411	22	AH15759
C	30	53	43.8	990	22	AH153612
C	31	53	43.8	1011	24	ABR92997
C	32	53	43.8	3330	22	AH54339
C	33	53	43.8	3532	22	AH54789
C	34	53	43.8	10822138	21	AAF22305
C	35	52	43.0	1272	25	ABT14859
C	36	52	43.0	1987	18	AVV74833
C	37	52	43.0	4352	23	ABJ02704
C	38	52	43.0	5519	23	ABZ29144
C	39	52	43.0	26270	21	AJZ46355
C	40	51	42.1	383	25	ASX20125
C	41	51	42.1	412	24	ABJ77577
C	42	51	42.1	502	24	ABP54633
C	43	51	42.1	505	24	ABV76729
C	44	51	42.1	592	24	ABO60296
C	45	51	42.1	1415	24	AEK84479

ALIGNMENTS

RESULT 1	DT	18-APR-2001 (first entry)
ID	XX	AAF56506 Standard; cDNA; 2401 BP.
DB	XX	Arabidopsis CDC27B
KW	XX	Cell cycle regulation; DNA replication; CDC7; CDC27A1; CDC27B; nematoe resistance; endoreduplication; sterility; polyploidy; SS.
OS	XX	Arabidopsis thaliana.
PN	XX	WO200102430-A2.

XX Hemerly AS, Ferreira PCG, Rombauts S;
 PD PI
 XX XX
 XX WPI; 2001-123101/13.
 PR Partially purified plant CDC27 or CDC7 protein homolog, useful for modulating DNA replication and for producing transgenic plants -
 XX PT
 PA PT
 (CROP-) CRODESIGN NV.
 FA (UVR-) UNIV RIO DE JANEIRO.
 XX P1
 Hemerly AS, Ferreira PCG, Rombauts S;
 DR Page 76-77; 86pp; English.
 XX
 PR Partially purified plant CDC27 or CDC7 protein homolog, useful for modulating DNA replication and for producing transgenic plants -
 XX P1
 PA Page 13; Page 85-86; 86pp; English.
 XX
 CC The present invention provides the protein and coding sequences of several Arabidopsis thaliana proteins which are involved in DNA replication and the regulation of the cell cycle. These include CDC7, CDC27A1, CDC27A2 and CDC27B. They are useful in the production of transgenic and mutant plants, as the mutations in the gene cause proteins to confer nematode resistance, sterility and polyploidy on plants and also lead to endoreduplication.
 XX
 SQ Sequence 2434 BP; 755 A; 475 C; 520 G; 684 T; 0 other;
 XX
 CC The present invention provides the protein and coding sequences of several Arabidopsis thaliana proteins which are involved in DNA replication and the regulation of the cell cycle. These include CDC7, CDC27A1, CDC27A2 and CDC27B. They are useful in the production of transgenic and mutant plants, as the mutations in the gene cause proteins to confer nematode resistance, sterility and polyploidy on plants and also lead to endoreduplication.
 XX
 SQ Sequence 2401 BP; 747 A; 466 C; 514 G; 674 T; 0 other;
 XX
 CC The present invention provides the protein and coding sequences of several Arabidopsis thaliana proteins which are involved in DNA replication and the regulation of the cell cycle. These include CDC7, CDC27A1, CDC27A2 and CDC27B. They are useful in the production of transgenic and mutant plants, as the mutations in the gene cause proteins to confer nematode resistance, sterility and polyploidy on plants and also lead to endoreduplication.
 XX
 SQ Sequence 2401 BP; 747 A; 466 C; 514 G; 674 T; 0 other;
 XX
 CC The present invention provides the protein and coding sequences of several Arabidopsis thaliana proteins which are involved in DNA replication and the regulation of the cell cycle. These include CDC7, CDC27A1, CDC27A2 and CDC27B. They are useful in the production of transgenic and mutant plants, as the mutations in the gene cause proteins to confer nematode resistance, sterility and polyploidy on plants and also lead to endoreduplication.

US-10-036-492-6 (1-24) x AAP56505 (1-2434)

Alignment Scores:
 Pred. No.: 2.93e-09 Length: 2434
 Score: 121.00 Matches: 24
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-10-036-492-6 (1-24) x AAP56505 (1-2434)

RESULT 3
 ABK93343
 ID ABK93343 standard; cDNA; 486 BP.
 XX ABK93343;
 AC
 DT 23-AUG-2002 (first entry)
 XX
 DE DNA encoding cell cycle regulation protein HOBBIT (HBT) #3.
 XX
 KW Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry; gene; ss.
 XX
 OS Arabidopsis thaliana.
 PN WO200238599-A2.
 XX
 DE 16-MAY-2002.
 XX
 PR 13-NOV-2001; 2001WO-EP11116.
 XX
 PR 13-NOV-2000; 2000EP-0870271.
 PR 30-NOV-2000; 2000US-250402P.
 XX
 PA (UYT-) RIJKSUNIV UTRECHT.
 XX
 PI Scheres BJJ, Blilou I, Folmer SDH;
 XX
 DR WPI; 2002-490065/52.
 DR P-PSDB; AB365520.

QY 1 valAsnLeuGlnLeuLeuAlaArgCystYleuSerIleuSerGlnAlaTyrSerAlaTyr 20
 DB 109 GTGAACTCCAATGTGTTACCCAGTGTAAGCTAACAGTCAGTAACTGAT 168

QY 21 TyrIleLeuLys 24
 DB 169 TATATCCCTAAA 180

RESULT 2
 AAP56505
 ID AAP56505 standard; cDNA; 2434 BP.
 XX
 AC AAP56505;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Arabidopsis CDC27A1 coding sequence.
 XX
 KW Cell cycle regulation; DNA replication; CDC7; CDC27A1; CDC27A2;
 KW CDC27B; nematode resistance; endoreduplication; sterility;
 KW polyploidy; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200102430-A2.
 XX
 PD 11-JAN-2001.
 XX
 PR 05-JUL-2000; 2000WO-EP06401.
 XX
 PR 05-JUL-1999; 99EP-0202214.
 XX
 PA (CROP-) CRODESIGN NV.
 PA (UVR-) UNIV RIO DE JANEIRO.

XX Use of plant cdc27B for modulating or mimicking auxin-related effects
 PR in plants or plant cells, or for regulation of cell cycle of plant cell
 PT
 XX
 PS Claim 31; Page 143; 207pp; English.

XX The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or altered pattern formation in a plant results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues; and/or a modification of the rate of organ or tissue emanation from a plant meristem; and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate under drought conditions; increase of seedling emergence; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues; and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes an *Arabidopsis thaliana* HOBBIT (HBT) or cdc27B protein described in the invention.

XX Sequence 486 BP; 132 A; 108 C; 102 G; 144 T; 0 other;

SQ Alignment Scores:
 Pred. No.: 2.33e-05 Length: 486
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indexes: 0
 DB: 24 Gaps: 0

US-10-036-492-6 (1-24) x ABK3343 (1-486)

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 106 GTTAATTGGAGCTATTAGCCACCAAGCTACCTGCAGATAATCAGCTTACAGTCATAT 165

QY 21 TyrIleLeuLys 24
 Db 166 CATCGCTAAG 177

RESULT 4

ABK3344 Length: 498
 ID ABK3344 standard CDNA: 498 BP.

XX AC ABK3344;

DT 23-AUG-2002 (first entry)

DB DNA encoding cell cycle regulation protein HOBBIT (HBT) #4.

XX Plant: cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry; gene; ss.

XX OS *Arabidopsis thaliana*.
 PR XX
 PN WO200238559-A2.
 XX
 PD 16-MAY-2002.

XX FF 13-NOV-2001; 2001WO-EPI3116.
 CC PR 13-NOV-2000; 2000EP-0870271.
 CC PR 30-NOV-2000; 2000US-256102P.
 CC XX (UYT-) RIJKSUNIV UTRECHT.

CC PA
 PI Scheres BJJ, Blilou I, Fomer SDH;
 XX
 DR WPI; 2002-49065/52.
 P-PDB: ABG65521.

XX PT Use of plant cdc27B for modulating or mimicking auxin-related effects in plants or plant cells, or for regulation of cell cycle of plant cell -
 PT -
 PT -
 PT -
 XX
 PS Claim 31; Page 144; 207pp; English.

XX The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or altered pattern formation in a plant results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues; and/or a modification of the arrangement of organs from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate under drought conditions; an enhanced shade avoidance response; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: increased survival rate under drought conditions; an increased shade avoidance response; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues; and/or the modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes an *Arabidopsis thaliana* HOBBIT (HBT) or cdc27B protein described in the invention.

XX Sequence 498 BP; 136 A; 105 C; 148 T; 0 other;

SQ Alignment Scores:
 Pred. No.: 2.4e-05 Length: 498
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indexes: 0
 DB: 24 Gaps: 0

US-10-036-492-6 (1-24) x ABK3344 (1-498)

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
 DB 106 GTTAATTGGAGCTATTAGCCACCAAGCTACCTGCAGATAATCAGCTTACAGTCATAT 165

QY 21 TyrIleLeuLys 24

DB 166 CATCGCTAAG 177

RESULT 5
 ABK93357 standard; cDNA; 1557 BP.
 XX
 AC
 XX
 DT 23-AUG-2002 (first entry)
 XX DNA encoding functionally inactive HOBBIT (HBT) protein #13.
 XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate;
 XX pattern formation; plant meristem development; plant yield; drought;
 XX vascular strand formation; root generation; shade avoidance response;
 XX cell cycle regulation; endoreduplication; patterning; parthenocarpic fruit;
 XX transgenic plant; plant development; plant morphology; plant physiology;
 XX plant biochemistry; gene; ss.
 XX Arabidopsis thaliana.
 OS XX WO200238599-A2.
 PN XX PD 16-MAY-2002.
 XX PP 13-NOV-2001; 2001WO-EPI13116.
 XX PR 13-NOV-2000; 2000EP-0870271.
 PR 30-NOV-2000; 2000US-250402P.
 PA (UYT-) RIJKSUNIV Utrecht.
 XX PI Scheres BJJ, Blilou I, Polymer SDH;
 DR WPI; 2002-490065/52.
 XX PR Use of Plant cdc27B for modulating or mimicking auxin-related effects
 PR in plants or plant cells, or for regulation of cell cycle of plant cell
 PR PS Claim 36; Page 176-177; 207pp; English.
 XX CC The invention described the use of a plant cdc27B (also termed HOBBIT
 CC (HBT)) useful for modulating or mimicking auxin-related effects in a
 CC plant or plant cell. The modulation or mimicking of auxin-related effects
 CC results in altered cell fate and/or altered pattern formation in a plant
 CC or plant cell; alteration in the size and/or number of naturally
 CC occurring plant meristems; modification of the numbers of organs or
 CC tissues, and/or a modification of the rate of organ or tissue emanation
 CC from a plant meristem, and/or a modification of the arrangement of organs
 CC and/or tissues in a plant; increased plant yield; an increased survival
 CC rate of plants; an enhanced survival rate under drought conditions;
 CC increase of seedling emergence; mimicking of root generation in tissue
 CC cultures; an increased shade avoidance response; production of parthenocarpic
 CC fruits. HBT also regulates the cell cycle of the plant cell results in:
 CC modulated endoreduplication in a plant; modulation of sterility in
 CC plants; increasing the cell cycle or increase of the rate of cell
 CC division; alteration in the size of naturally occurring meristems; a
 CC modification in a number of organs or tissues, and/or the modification of
 CC the rate of organ or tissue emanation from a plant meristem and/or
 CC modification of the arrangement of the organs and/or tissues in a plant
 CC and/or an increased plant yield or enhancement of survival rate of
 CC plants. A nucleic acid encoding HBT is useful for producing transgenic
 CC plants, plant cells or plant tissues and in the regeneration of a plant
 CC from a plant cell. HBT nucleic acids and proteins are useful for
 CC modifying cell fate, pattern formation, plant development, plant
 CC morphology, plant physiology and/or plant biochemistry. This sequence
 CC encodes a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or
 CC cdc27B protein described in the invention.

Sequence 1557 BP; 448 A; 339 C; 328 G; 442 T; 0 other;

XX SQ

Alignment Scores:
 Pred. No.: 9.58e-05
 Score: 91.00
 Percent Similarity: 87.50%
 Best Local Similarity: 75.00%
 Query Match: 75.21%
 DB: 24
 DB:

Length: 1557
 Matches: 18
 Conservatives: 3
 Mismatches: 3
 Indels: 0
 Gaps: 0

US-10-036-492-6 (1-24) x ABK93357 (1-1557)

Qy 1 ValAsnLeuGlnLeuLeuAlaArgCysteyleuSerAsnSerGlnAlaTyrSerAlaTyr 20
Db 106 GTTATTGCACTATTGCCACAGTACTCGAAGATAATCAAGCTTACAGTGATAT 165

Qy 21 TyrIleLeuIys 24
Db 166 CATCTGCTAAAG 177

RESULT 6
 ABK93356 standard; cDNA; 2115 BP.
 ID ABK93356
 XX XX DE 23-AUG-2002 (first entry)
 XX XX DE DNA encoding functionally inactive HOBBIT (HBT) protein #12.
 XX XX DE Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate;
 XX pattern formation; plant meristem development; plant yield; drought;
 XX seedling emergence; root generation; shade avoidance response;
 XX vascular strand formation; patterning; parthenocarpic fruit;
 XX cell cycle regulation; endoreduplication; cell division;
 XX transgenic plant; plant development; plant morphology; plant physiology;
 XX plant biochemistry; gene; ss.
 XX CS Arabidopsis thaliana.
 XX PN WO200238599-A2.
 XX PD 16-MAY-2002.
 XX PR 13-NOV-2001; 2001WO-EPI13116.
 XX PR 13-NOV-2000; 2000EP-0870271.
 PR 30-NOV-2000; 2000US-250402P.
 PA (UYT-) RIJKSUNIV Utrecht.
 XX PI Scheres BJJ, Blilou I, Polymer SDH;
 DR WPI; 2002-490065/52.
 XX PR Use of Plant cdc27B for modulating or mimicking auxin-related effects
 PR in plants or plant cells, or for regulation of cell cycle of plant cell
 PR PS Claim 36; Page 175-176; 207pp; English.

CC The invention described the use of a plant cdc27B (also termed HOBBIT
CC (HBT)) useful for modulating or mimicking auxin-related effects in a
CC plant or plant cell. The modulation or mimicking of auxin-related effects
CC results in altered cell fate and/or altered pattern formation in a plant
CC or plant cell; alteration in the size and/or number of naturally
CC occurring plant meristems; modification of the numbers of organs or
CC tissues, and/or a modification of the rate of organ or tissue emanation
CC from a plant meristem, and/or a modification of the arrangement of organs
CC and/or tissues in a plant; increased plant yield; an increased survival
CC rate of plants; an enhanced survival rate under drought conditions;
CC increase of seedling emergence; mimicking of root generation in tissue
CC cultures; an increased shade avoidance response; production of parthenocarpic
CC fruits. HBT also regulates the cell cycle of the plant cell results in:
CC modulated endoreduplication in a plant; modulation of sterility in
CC plants; increasing the cell cycle or increase of the rate of cell
CC division; alteration in the size of naturally occurring meristems; a
CC modification in a number of organs or tissues, and/or the modification of
CC the rate of organ or tissue emanation from a plant meristem and/or
CC modification of the arrangement of the organs and/or tissues in a plant
CC and/or an increased plant yield or enhancement of survival rate of
CC plants. A nucleic acid encoding HBT is useful for producing transgenic
CC plants, plant cells or plant tissues and in the regeneration of a plant
CC from a plant cell. HBT nucleic acids and proteins are useful for
CC modifying cell fate, pattern formation, plant development, plant
CC morphology, plant physiology and/or plant biochemistry. This sequence
CC encodes a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or
CC cdc27B protein described in the invention.

CC Sequence 1557 BP; 448 A; 339 C; 328 G; 442 T; 0 other;

CC SQ

The invention described the use of a plant cdc27B (also termed HOBBIT
CC (HBT)) useful for modulating or mimicking auxin-related effects in a
CC plant or plant cell. The modulation or mimicking of auxin-related effects
CC results in altered cell fate and/or altered pattern formation in a plant
CC or plant cell; alteration in the size and/or number of naturally
CC occurring plant meristems; modification of the numbers of organs or
CC tissues, and/or a modification of the rate of organ or tissue emanation
CC from a plant meristem, and/or a modification of the arrangement of organs
CC and/or tissues in a plant; increased plant yield; an increased survival
CC rate of plants; an enhanced survival rate under drought conditions;
CC increase of seedling emergence; mimicking of root generation in tissue
CC cultures; an increased shade avoidance response; production of parthenocarpic
CC fruits. HBT also regulates the cell cycle of the plant cell results in:
CC modulated endoreduplication in a plant; modulation of sterility in
CC plants; increasing the cell cycle or increase of the rate of cell
CC division; alteration in the size of naturally occurring meristems; a
CC modification in a number of organs or tissues, and/or the modification of
CC the rate of organ or tissue emanation from a plant meristem and/or
CC modification of the arrangement of the organs and/or tissues in a plant
CC and/or an increased plant yield or enhancement of survival rate of
CC plants. A nucleic acid encoding HBT is useful for producing transgenic
CC plants, plant cells or plant tissues and in the regeneration of a plant
CC from a plant cell. HBT nucleic acids and proteins are useful for
CC modifying cell fate, pattern formation, plant development, plant
CC morphology, plant physiology and/or plant biochemistry. This sequence
CC encodes a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or
CC cdc27B protein described in the invention.

CC Sequence 1557 BP; 448 A; 339 C; 328 G; 442 T; 0 other;

CC SQ

The invention described the use of a plant cdc27B (also termed HOBBIT
CC (HBT)) useful for modulating or mimicking auxin-related effects in a
CC plant or plant cell. The modulation or mimicking of auxin-related effects
CC results in altered cell fate and/or altered pattern formation in a plant
CC or plant cell; alteration in the size and/or number of naturally
CC occurring plant meristems; modification of the numbers of organs or
CC tissues, and/or a modification of the rate of organ or tissue emanation
CC from a plant meristem, and/or a modification of the arrangement of organs
CC and/or tissues in a plant; increased plant yield; an increased survival
CC rate of plants; an enhanced survival rate under drought conditions;
CC increase of seedling emergence; mimicking of root generation in tissue
CC cultures; an increased shade avoidance response; production of parthenocarpic
CC fruits. HBT also regulates the cell cycle of the plant cell results in:

CC modulated endoreduplication in a plant; modulation of sterility in
 CC plants; increasing the cell cycle or increase of the rate of cell
 CC division; alteration in the size of naturally occurring meristems; a
 CC modification in number of organs or tissues, and/or the modification of
 CC the rate of organ or tissue emanation from a plant meristem and/or
 CC modification of the arrangement of the organs and/or tissues in a plant
 CC and/or an increased plant yield or enhancement of survival rate of
 CC plants. A nucleic acid encoding HBT is useful for producing transgenic
 CC plants, plant cells or plant tissues and in the regeneration of a plant
 CC from a plant cell. HBT nucleic acids and proteins are useful for
 CC modifying cell fate, pattern formation, plant development, plant
 CC morphology, plant physiology and/or plant biochemistry. This sequence
 CC encodes a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or
 CC cdc27B protein described in the invention.

XX Sequence 2115 BP; 634 A; 450 C; 458 G; 573 T; 0 other;

Alignment Scores:	
Pred. No. :	0.009139
Score:	91.00
Percent Similarity:	87.50%
Best Local Similarity:	75.00%
Query Match:	75.21%
DB:	24
Length:	2115
Matches:	18
Conservative:	3
Mismatches:	0
Indels:	0
Gaps:	0

US-10-036-492-6 (1-24) x ABK93356 (1-2115)

QY 1 ValLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
 Db 106 GTTAATTGGAGCPATTAGCACCAGCTACCTGCAGATAATCGACTGTCAAT 165

QY 21 TyrIleLeuIys 24
 Db 166 CATCGCTAAAG 177

RESULT 7
 ABK93355 ID ABK93355 standard; CDNA; 2169 BP.
 XX AC ABK93355;
 XX DT 23-AUG-2002 (first entry)
 XX DE DNA encoding functionally inactive HOBBIT (HBT) protein #11.
 XX Plant: cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate;
 KW plant formation; plant meristem development; plant yield; drought;
 KW seedling emergence; root generation; shade avoidance response;
 KW vascular strand formation; patterning; parthenocarpic fruit;
 KW cell cycle regulation; endoreduplication; cell division;
 KW transgenic plant; plant development; plant morphology; plant physiology;
 KW plant biochemistry; gene; ss.

OS Arabidopsis thaliana.
 XX WO200238599-A2.

XX PD 16-MAY-2002.

XX PF 13-NOV-2001; 2001WO-EP13116.
 XX PR 13-NOV-2000; 2000EP-0870271.
 XX 30-NOV-2000; 2000US-250402P.
 XX PA (UYUT-) RIJKSUNIV Utrecht.

XX Scheres BJJ, Blilou I, Polymer SDH;
 XX WPI: 2002-490065/52.

XX Use of plant cdc27B for modulating or mimicking auxin-related effects
 PR in plants or plant cells, or for regulation of cell cycle of plant cell
 PR -

XX Claim 36; Page 174-175; 207pp; English.

PS The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate of plants; an enhanced survival rate under drought conditions; increase of seedling emergence; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.

XX SQ Sequence 2169 BP; 643 A; 462 C; 470 G; 594 T; 0 other;

XX Alignment Scores:
 Pred. No. : 0.009143 Length: 2169
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 24 Gaps: 0

XX US-10-036-492-6 (1-24) x ABK93355 (1-2169)
 XX Alignment Scores:
 Pred. No. : 0.009143 Length: 2169
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 24 Gaps: 0

XX QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
 XX Db 106 GTTAATTGGAGCPATTAGCACCAGCTACCTGCAGATAATCGACTGTCAAT 165

XX QY 21 TyrIleLeuIys 24
 XX Db 166 CATCGCTAAAG 177

RESULT 8

AAF56507 ID AAF56507 standard; CDNA; 2220 BP.
 XX AC AAF56507;
 XX DT 18-APR-2001 (first entry)
 XX DE Arabidopsis Cdc27B coding sequence.
 XX KW Cell cycle regulation; DNA replication; CDC27; CDC27A1; CDC27A2;
 KW CDC27B; nematode resistance; endoreduplication; sterility;
 KW polyploidy; ss.

XX OS Arabidopsis thaliana.
 XX WO200102430-A2.

XX PN WO200102430-A2.
 XX PD 11-JAN-2001.
 XX PF 05-JUL-2000; 2000WO-EP06401.

XX Scheres BJG, Blilou I, Folmer SDH;
 PR PI
 XX XX
 PA (CROP-) CRODESIGN NV.
 PA (TYRI-) UNIV RIO DE JANEIRO.
 XX Use of plant cdc27B for modulating or mimicking auxin-related effects
 PT in plants or plant cells, or for regulation of cell cycle of plant cell
 PT
 DR WPI; 2001-123104/13.
 XX PS Claim 31; Page 142-143; 207pp; English.

PR Partially purified plant CDC27 or CDC7 protein homolog, useful for
 PT modulating DNA replication and for producing transgenic plants -
 XX
 PS Claim 13; Page 86; 86pp; English.

CC The present invention provides the protein and coding sequences of
 several Arabidopsis thaliana proteins which are involved in DNA
 replication and the regulation of the cell cycle. These include CDC7,
 CDC27A1, CDC27A2 and CDC27B. They are useful in the production of
 transgenic and mutant plants, as the mutations in the gene cause
 proteins to confer nematode resistance, sterility and polyploidy on
 plants and also lead to endoreduplication.

XX Sequence 22220 BP; 658 A; 474 C; 480 G; 608 T; 0 other;

CC Alignment Scores:
 Prd. No.: 0.000147 Length: 2220
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 22 Gaps: 0

US-10-036-492-6 (1-24) × ABK93342 (1-2220)

QY 1 ValAsnLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrSerAlaTyr 20
 DB 106 GTPATTCAGCTATTGCCACAGCTACCTGCAGATAATCAAGTACAGTGATAT 165

QY 21 TyrIleLeuLys 24
 DB 166 CATCGCTAAAG 177

RESULT 9

ID ABK93342 Standard; cDNA; 2235 BP.

XX ABK93342; 23-AUG-2002 (first entry)

DE DNA encoding cell cycle regulation protein HOBBIT (HBT) #2.

XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry; gene; ss.

XX Arabidopsis thaliana.

OS WO200235599-A2.

PN XX

PD 16-MAY-2002.

XX 13-NOV-2001; 2001WO-EPI3116.

PF XX

PR 13-NOV-2000; 2000EP-0870271.

PR 30-NOV-2000; 2000JS-251402P.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX

XX Scheres BJG, Blilou I, Folmer SDH;

PI PI
 XX XX
 DR WPI; 2002-490065/52.

XX Use of plant cdc27B for modulating or mimicking auxin-related effects
 PT in plants or plant cells, or for regulation of cell cycle of plant cell
 PT
 XX PS Claim 31; Page 142-143; 207pp; English.

CC The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell rate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem; and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate of plants; an enhanced survival rate of plants; an increased survival rate under drought conditions; increase of seedling emergence; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes an Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.

XX SQ Sequence 2235 BP; 664 A; 475 C; 484 G; 612 T; 0 other;

CC Alignment Scores:
 Pred. No.: 0.000149 Length: 2235
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 24 Gaps: 0

US-10-036-492-6 (1-24) × ABK93342 (1-2235)

QY 1 ValAlaLeuGlnLeuAlaArgCystYleSerAsnSerGlnAlaTyrLeuLeuAlaArgCystYleSerAlaTyr 20
 DB 106 GTTAATTGGAGCTTACCTGCACAGCTACCTGCAGATAATCAAGCTAACGCTTACAGTGCTAT 165

QY 21 TyrIleLeuLys 24
 DB 166 CATCGCTAAAG 177

RESULT 10

ID ABK93352 Standard; cDNA; 2235 BP.

XX ABK93352; 23-AUG-2002 (first entry)

DE DNA encoding functionally inactive HOBBIT (HBT) protein #8.

XX DNA encoding functionally inactive HOBBIT (HBT) protein #8.

XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry; gene; ss.

XX Arabidopsis thaliana.

OS WO200235599-A2.

PN XX

PD 16-MAY-2002.

XX 13-NOV-2001; 2001WO-EPI3116.

PF XX

PR 13-NOV-2000; 2000EP-0870271.

PR 30-NOV-2000; 2000JS-251402P.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX

KW	vascular strand formation; patterning; parthenocarpic fruit;	QY	21 TyrIleLeuLys 24
KW	cell cycle regulation; endoreduplication; cell division;	Db	:::::
KW	transgenic plant; Plant development; Plant morphology; plant physiology;		166 CATTGCTAAAG 177
KW	plant biochemistry; gene; ss.		
XX	Arabidopsis thaliana.	RESULT 11	
OS		ID ABK93354 standard; cDNA; 2235 BP.	
XX	WO20028599-A2.	XX	ABK93354;
XX	PD 16-MAY-2002.	XX	AC
XX	PF 13-NOV-2001; 2001WO-EP131116.	DT 23-AUG-2002 (first entry)	
XX	PR 13-NOV-2000; 2000EP-06702271.	DE DNA encoding functionally inactive HOBBIT (HBT) protein #10.	
XX	PR 30-NOV-2000; 2000US-250402P.	XX	Plant: cdc27B; Cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry; gene; ss.
PA (UYUT-) RIJKSUNIV UTRECHT.	PR	XX	KW
XX	Scheres BUG, Blilou I, Folmer SDH; DR; 2002-490065/52.	XX	KW
PR	Use of plant cdc27B for modulating or mimicking auxin-related effects in plants or plant cells, or for regulation of cell cycle of plant cell	XX	KW
PR	-	XX	KW
PS	Claim 36; Page 170-171; 207pp; English.	PN WO200238599-A2.	
XX	The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate of plants; an increased survival rate of plants; an enhanced survival conditions; increase of seedling emergency; mimicking of root generation in tissue cultures; an increased shade avoidance response; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants; plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes functionally inactive Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.	XX	Claim 36; Page 172-174; 207pp; English.
CC	Sequence 2235 BP; 664 A; 474 C; 484 G; 613 T; 0 other:	XX	The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate under drought conditions; increase of seedling emergency; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation; and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants; plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes functionally inactive Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.
CC	Alignment Scores:	XX	CC
Ped. No.:	0.000149	Length:	2235
Score:	91.00	Matches:	18
Percent Similarity:	87.50%	Conservative:	3
Best Local Similarity:	75.00%	Mismatches:	3
Query Match:	75.21%	Indels:	0
DB:	24	Gaps:	
US-10-036-492-6 (1-24) x ABK93352 (1-2235)	1 ValAsnLeuGlnLeuLeuAlaArgCystYLeuSerAsnSerGlnAlaTyrsAlaYyr 20	CC	CC
Oy	1 GTRATTGAGCTATGGCAAGCTTACCTGAGATAACGTTACGTGCATAT 165	CC	CC
Db	106 GTRATTGAGCTATGGCAAGCTTACCTGAGATAACGTTACGTGCATAT 165	CC	CC

PPT Use of plant *cdc27B* for modulating or mimicking auxin-related effects in plants or plant cells, or for regulation of cell cycle of plant cell

Claim 36; Page 171-172; 207pp; English.

The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organ and/or tissues in a plant; increased plant yield; an increased survival rate of plants; an enhanced survival rate under drought conditions; increase of seedling emergence; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular structure and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence cdc27B protein described in the invention is a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or

Sentence 2313 RD: 682 2: 493 C: 494 G: 644 T: 0 other:

Alignment Scores:	
Pred. No. :	0.000155
Score:	91.00
Percent Similarity:	87.50%
Best Local Similarity:	75.00%
Query Match:	75.21%
DR.	24
Length:	2313
Matches:	18
Conservative:	3
Mismatches:	3
Indels:	0
Gaps:	0

US-10-036-492-6 (1-24) x AB93353 (1-2313)

21 Tyrileleuys 24

RESULT 14 AAC50257

xx

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99US-01420555

plant biochemistry; gene; ss.
 XX Arabidopsis thaliana.
 OS WO200238599-A2.
 PN XX
 PD XX 16-MAY-2002.
 PF XX 13-NOV-2001; 2001WO-EP131116.
 PR XX 13-NOV-2000; 2000EP-0870271.
 PR 30-NOV-2000; 2000US-256402P.
 PA XX (UYUT-) RIJKSUNIV Utrecht.
 PT PI Scheres BJJ, Billiou I, Polymer SDH;
 XX DR WPI; 2002-490065/52.

XX Use of plant cdc27B for modulating or mimicking auxin-related effects
 PR in plants or plant cells, or for regulation of cell cycle of plant cell
 PR
 PS XX

Claim 31; Page 140-142; 207pp; English.

XX The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased plant yield; an increased survival rate of plants; an enhanced survival rate under drought conditions; increase of seedling emergence; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This sequence encodes an Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.

XX Sequence 2480 BP; 737 A; 527 C; 533 G; 683 T; 0 other;

Alignment Scores:			
Pred. No.:	0.000169	Length:	2480
Score:	91.00	Matches:	18
Percent Similarity:	87.50%	Conservative:	3
Best Local Similarity:	75.00%	Mismatches:	3
Query Match:	75.21%	Indels:	0
DB:	24	Gaps:	0

US-10-036-492-6 (1-24) x ABK93341 (1-2480)

Qy	1 ValAsnLeuGlnLeuLeuAlaArgCystTyrIleSerAsnSerGlnAlaTyrSerAlaTyr 20
Db	121 GTTAATTGCACTATAGCCACGGTACCTGCAAGATAATCAAGCTAACGTGCAAT 180
Qy	21 TyrIleLeuLys 24
Db	181 CATCTGCTAAAG 192

Predec. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3

Result No.	Query Score	Match Length	DB ID	Description
1	121	100.0	AX068991	AX068991 Sequence
2	121	100.0	AX068986	AX068986 Sequence
3	121	100.0	ABD23046	Arabidopsis thaliana
c	121	100.0	AC001645	Arabidopsis thaliana
c	121	100.0	AC001645	Arabidopsis thaliana
5	91	135457	AC084820	Arabidopsis thaliana
6	91	75.2	AX42180	Arabidopsis thaliana
7	91	75.2	498	AX462181 Sequence
8	91	75.2	1557	AX462198 Sequence
9	91	75.2	1915	AX428780 Sequence
10	91	75.2	2115	AX462197 Sequence
11	91	75.2	2169	AX462196 Sequence
12	91	75.2	2220	AX068992 Sequence
13	91	75.2	2225	AX462179 Sequence
14	91	75.2	2235	AX462193 Sequence
15	91	75.2	2235	AX462195 Sequence
16	91	75.2	2235	AX462199 Sequence
17	91	75.2	2313	AX462194 Sequence
18	91	75.2	2480	AX462178 Sequence
19	91	75.2	2672	AX062470 Sequence
20	91	75.2	2877	ATHA.897659 Sequence
21	91	75.2	4577	AX462176 Sequence
22	91	75.2	4577	AX462186 Sequence
23	91	75.2	4577	AX462187 Sequence
24	91	75.2	4577	AX462188 Sequence
25	91	75.2	4577	AX462189 Sequence
26	91	75.2	4577	AX462190 Sequence
27	91	75.2	4577	AX462191 Sequence
28	91	75.2	4577	AX462192 Sequence
29	91	75.2	97814	AC006081 Arabidopsis thaliana
30	87	71.9	140327	AP03938 Oryza sativa
31	87	71.9	173297	AP003539 Oryza sativa
32	63	52.1	2995	BC049466 Danio rerio
c	33	61	50.4	73450 AC137580 Homo sapiens
c	34	61	50.4	149041 AC044782 Homo sapiens
c	35	61	50.4	179789 AC009543 Homo sapiens
c	36	61	50.4	189092 GTA110592 Homo sapiens
c	37	59	48.8	BD05555 BD05555 Sequence
c	38	59	48.8	BC023187 BC023187 Mus musculus
39	59	48.8	1864 10	I1768 Sequence 1'
40	59	48.8	2472 6	U0001 Human homolog
41	59	48.8	2592 9	BC0165 Homo sapiens
42	59	48.8	3320 9	S78234 nuc2 Homo sapiens
c	43	59	48.8	53128 2 AC0898237 Homo sapiens
c	44	59	48.8	675610 AC002558 Homo sapiens
45	59	48.8	102064 9 AC002558 Homo sapiens	

ATTACHMENT

DEPARTMENT 1

AX068991 AX068991 2401 bp DNA linear PAT 25-JAN-2001 DB: US-10-036-492-6 (1-24) x AX068986 (1-2434)

LOCUS Sequence 14 from Patent WO0102430.

DEFINITION AX068991

ACCESSION AX068991

VERSION GI:12578821

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1. Hemery,A.S., Ferreira,P.C. and Rombauts,S.

AUTHORS Arabidopsis thaliana cdc7 and cdc27 homologs

TITLE Patent: WO 0102430-A 14-11-JAN-2001;

CropDesign N.V. (BE) ; Universidade Federal do Rio de Janeiro (BR)

JOURNAL

FEATURES Location/Qualifiers

source 1..2401

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

BASE COUNT 747 a 466 c 514 g 674 t

ORIGIN

Alignment Scores:

Pred. No. :	2.26e-10	Length:	2401
Score:	121.00	Matches:	24
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-036-492-6 (1-24) x AX068991 (1-2401) 1.

Qy 1 valAsnLeuGlnIleLeuAlaArgCYSerLeuSerSerGlnAlaTyrSerAlaTyr 20

Db 109 GTGAACTCGCAATGGTAGCCAGSTGTTACTTGAGTAACAGTCAAAGCTTATAAGTCATAT 168

Qy 21 TyrIleLeuIys 24

Db 169 TATATCCTTAA 180

RESULT 2

LOCUS Sequence 9 from Patent WO0102430.

DEFINITION AX068986

ACCESSION AX068986

VERSION GI:12578821

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1. Hemery,A.S., Ferreira,P.C. and Rombauts,S.

AUTHORS Arabidopsis thaliana cdc7 and cdc27 homologs

TITLE Patent: WO 0102430-A 9-11-JAN-2001;

CropDesign N.V. (BE) ; Universidade Federal do Rio de Janeiro (BR)

JOURNAL

FEATURES Location/Qualifiers

source 1..2414

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

BASE COUNT 755 a 475 c 520 g 684 t

ORIGIN

Alignment Scores:

Pred. No. :	2.29e-10	Length:	2434
Score:	121.00	Matches:	24
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

RESULTS

AB023046 Arabidopsis thaliana Genomic DNA, chromosome 3, PI clone: MYA6.

LOCUS AB023046

DEFINITION AB023046 BA000014

ACCESSION AB023046.1

VERSION GI:4220645

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids III; Brassicales; Brassicaceae; Arabidopsis.

1 (sites)

Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.

STRUCTURAL ANALYSIS OF ARABIDOPSIS THALIANA CHROMOSOME 3. I. SEQUENCING FEATURES OF THE REGIONS OF 4,504,864 BP COVERED BY SIXTY PI AND TAC CLONES DNA Res. 7 (2), 131-135 (2000)

REFERENCE

AUTHORS Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.

JOURNAL DNA Res.

MEDLINE 2027450

PUBMED 10819329

REMARKS 2 (bases 1 to 75289)

AUTHORS Direct Submission

JOURNAL

MEDLINE

PUBMED

COMMENT

For the latest information on annotation of this clone, Please see http://www.kazusa.or.jp/kao/cgi-bin/agd_graph.cgi?c=MYA6

Submitted (01-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kao@kazusa.or.jp

REFERENCE

AUTHORS For the latest information on annotation of this clone, Please see http://www.kazusa.or.jp/kao/cgi-bin/agd_graph.cgi?c=MYA6

JOURNAL

MEDLINE

PUBMED

COMMENT

Genes with similarity to proteins in the databases are described in 'product', or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCG-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebbgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Voller Brendel, Stanford University, http://gremlin.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding RNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

The 5' clone is NS1 and the 3' clone is MDC8.

LOCATION/QUALIFIERS

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/mol_type="Genomic DNA"

/clone="Mitsui_P1"

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unknown_protein"

/codon_start=1

/evidence=not_experimental
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 SGDBSKTKEPRHLYLLASNFLSRLGHWCKPNSRKEKEVNTISDILFLISTAFBHSFVCLP
 RFDPAIGCFGLDGLESDFRAGLPVNPCKRSEKIGEVEWTISDILKGGHLEEFPTIYETRP
 IKNMYYGNGFDSRSGLWMARWIKPDMMIEASFKGHTSWIROLAQMDDTPMISLTERH
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 KRQKQLAKGAFRHLIPEDDYTGDRGTDYSLRQICDQSHRGCHSCFKDSIARKSK
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 complement "(7397 . 8479)"
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 LPPLVYNGQFSSPLUGTQSQKLTGTYCNKEIRKGSWSKLISSMSFIS
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 gene_id:MYA6.120
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Best Local Similarity: 100.00% Missmatches: 0 FEATURES exons by GRAIL are annotated as misc features.

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LENVPRPPEPKSQYVGDDFQETGGAHPLAFEVGVNNKEAATIVQLMGCG
GSSAGGGKGKHSWLYLRINHQOQSCFTATNTGFGTGYCTSPFAQCGI
ELVASEMNAAVADGKVNKHDLRAKATKSAITMLNLIESMTIAEDIGRQLTYGERKRP
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complement(6086..6130)

/note="exon predicted by xgrail, quality marginal shadowexon"

6308..6436

/rpt_family="POLY_A"

complement(6535..6567)

/rpt_family="T_rich"

complement(6782..6887)

/note="exon predicted by xgrail, quality marginal shadowexon"

gene

mRNA

CDS

repeat_region

misc_feature

repeat_region

misc_feature

comment

Steve Rounseley
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Address all correspondence to:

USA

e-mail: rounseley@tigr.org

From Arthur Epmorn (gov), GeneFinder (Phil Green, University of Washington), Genscan (Chris Burge, Stanford.edu/~chris/GENSCAN.html), and NetPlantGene (http://www.cbs.dtu.dk/~neplgen/cbnetgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tcb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named as isologs. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/dby/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/Rh/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted

59159 * 60027: contig of 869 bp in length
 60128 * 6017: gap of unknown length
 60128 * 6087: contig of 749 bp in length
 6087: 60976: gap of unknown length
 60976: 61222: contig of 246 bp in length
 61223: 61322: gap of unknown length
 61323: 61192: contig of 580 bp in length
 62002: 62003: gap of unknown length
 62977: 62978: contig of 975 bp in length
 63078: 63078: gap of unknown length
 63986: 63987: contig of 809 bp in length
 63986: 64696: gap of unknown length
 64697: 64796: contig of 710 bp in length
 64796: 65406: gap of unknown length
 65406: 65506: contig of 610 bp in length
 65506: 65507: gap of unknown length
 65507: 66419: contig of 973 bp in length
 66480: 66579: gap of unknown length
 66580: 66856: contig of 287 bp in length
 66857: 66867: gap of unknown length
 66867: 66897: contig of 1617 bp in length
 68554: 68683: gap of unknown length
 68684: 69531: contig of 848 bp in length
 69532: 69631: gap of unknown length
 69632: 69808: contig of 177 bp in length
 69809: 69909: gap of unknown length
 69909: 70052: contig of 154 bp in length
 70052: 70163: gap of unknown length
 70163: 76438: contig of 6336 bp in length
 76598: 76599: gap of unknown length
 79332: 79332: contig of 2794 bp in length
 79332: 79432: gap of unknown length
 79432: 85433: contig of 6001 bp in length
 85433: 85594: gap of unknown length
 85594: 87441: contig of 1848 bp in length
 87442: 8751: gap of unknown length
 8751: 92881: contig of 5340 bp in length
 92881: 92982: gap of unknown length
 92982: 93835: contig of 854 bp in length
 93835: 93936: gap of unknown length
 93936: 94804: contig of 869 bp in length
 94804: 94904: gap of unknown length
 94904: 96100: contig of 1286 bp in length
 96100: 96200: gap of unknown length
 96200: 96291: contig of 39167 bp in length
 96291: 134547: contig of 39167 bp in length.

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 source 1. 134547
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /chromosome="1"
 /clone="P12P3"

BASE COUNT 42738 a 22476 c 23879 g 43123 t 3241 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1. 5.2e-08
 Score: 121.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB:

Length: 135457
 Matches: 24
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-036-492-6 (1-24) X AC084820 (1-134547)

Qy 1 ValAsnLeuGlnLeuLeuAlaArgCystYleuSerAsnSerGinAlaTyrSerAlaTyr 20

Db 70569 GTGAACCTGCATTGTAGCCAGGGTTACTTGATTAAGTCAGTCAAGTCATA 70510

Qy 21 TyrIleLeuLys 24

Db 70509 TATATCCTAAA 70498

RESULT 6
 AX462180
 LOCUS AX462180 Sequence 4 from Patent WO238599.
 DEFINITION AX462180
 ACCESSION AX462180.1 GI:2127743
 VERSION AX462180.1
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE ORGANISM Arabidopsis; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyt; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 Scheres, B.J., Blilou, I. and Folmer, S.D.
 AUTHORS A plant development regulating gene and its uses
 TITLE A Plant Development Regulating Gene and Its Uses
 JOURNAL Patent: WO 0238599-A 4-16-MAY-2002;
 Universiteit Utrecht (NL)
 FEATURES Location/Qualifiers
 source 1. 1. 486
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 BASE COUNT 132 a 108 c 102 g 144 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.71e-06
 Score: 91.00 Length: 486
 Percent Similarity: 87.50% Matches: 18
 Best Local Similarity: 75.00% Conservative: 3
 Query Match: 75.21% Mismatches: 3
 DB: 6 Indels: 0
 Gaps: 0
 US-10-036-492-6 (1-24) X AX462180 (1-486)
 Qy 1 ValAsnLeuGlnLeuLeuAlaArgCystYleuSerAsnSerGinAlaTyrSerAlaTyr 20
 Db 106 GTTAAATGCACTTAGCCACAGCTACCTGAGATAATCAGCTAACAGTGGAT 165
 FEATURES Location/Qualifiers
 source 1. 1. 498
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 BASE COUNT 136 a 109 c 105 g 148 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.83e-05 Length: 498
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3

Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 6 Gaps: 0

US-10-036-492-6 (1-24) x AX462181 (1-498)

Qy 1 ValAsnLeuGlnLeuAlaArgCysteTyLeuSerAsnSerGlnAlaTySerAlaTySerAlaTy 20
 Db 106 GTTAATTCGACTTATGCCACCGATTCTGCAGATAATCACGTACAGTGCTAT 165

RESULT: 8

AX462198 LCUS AX462198 DNA linear PAT 09-JUL-2002
 DEFINITION Sequence 22 from Patent WO0238599.
 ACCESSION AX462198
 VERSION AX462198.1 GI:21727757
 KEYWORDS SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana; Streptophytina; Embryophytina; Tracheophytina;
 Eukaryota; Viridiplantae; Magnoliophytina; eudicots; core eudicots;
 Spermatophytina; Brassicales; Brassicaceae; Arabidopsis; rosids; eurosids II; Brassicales; Arabidopsis.

REFERENCE 1. Scheres, B.J., Blilou, I. and Folmer, S.D.,
 AUTHORS A plant development regulating gene and its uses
 TITLE Patent: WO 02/8599-A 22 16-MAY-2002;
 JOURNAL Universiteit Utrecht (NL)
 Location/Qualifiers 1..1557

FEATURES source /organism="Arabidopsis thaliana"
 /mol type="genomic DNA"
 /db_xref="taxon:3702"
 BASE COUNT 448 a 339 c 328 g 442 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.59e-05 Length: 1557
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 6 Gaps: 0

US-10-036-492-6 (1-24) x AX462198 (1-1557)

Qy 1 ValAsnLeuGlnLeuAlaArgCysteTyLeuSerAsnSerGlnAlaTySerAlaTy 20
 Db 106 GTTAATTCGACTTATGCCACCGATTCTGCAGATAATCACGTACAGTGCTAT 165

RESULT: 8

AX462198 LCUS AX462198 DNA linear PLN 07-AUG-2002
 DEFINITION Arabidopsis thaliana CDC27/NCIC2-like protein (At2g20000) mRNA,
 complete cds.
 ACCESSION AY126780
 VERSION AY126780.1 GI:22136203
 KEYWORDS SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana; Streptophytina; Embryophytina; Tracheophytina;
 Eukaryota; Viridiplantae; Magnoliophytina; eudicots; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1915) FLI C DNA.
 AUTHORS Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M.,
 Palm, C.J., Bowser, L., Jones, T., Bath, J., Carninci, P., Chen, H.,

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

TITLE JOURNAL Direct Submission
 Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA

COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of R AFLP DNAs (R AFLP cDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

COMMENT The Salk, Stanford, PGEC (SP) Consortium members constructed and
 sequenced the RPN1 (ORF) clones using the R AFLP DNAs: Tripp,M.,
 Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Bath,J., Chen,H., Cheuk,R.,
 Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H.,
 Shian,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
 Tripp,M. (SP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
 to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
 (SP/Stanford) contributed equally to this work as PIs.

FEATURES Location/Qualifiers 1..1915
 source /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /chromosome="2"
 /clone="U12304"
 /note="This clone is in PENTR/SD-dtopo. This is a cloned
 PCR product using RIKEN clone RAFL07-12-N15 (AY062470) as
 a template." ecotype: "columbia"
 gene 1..1915
 /gene="At2g20000"
 /note="Synonym: T2G17.20"
 CDS 1..1416
 /gene="At2g20000"
 /codon_start=1
 /product="CDC27/NCIC2-like protein"
 /protein_id="AAH91180.1"
 /db_xref="GI: 22136204"
 /translation="MEAMLYDVCVANSRLRHEVKKALPFMCERLCAFPSSPVNLQLLATS
 YLNQNQYSATVLLKGTOMAQSRSLCFMDLINEALCPVNPGAEIPNGAA
 GHYLGHIIKYKTDRRNAAQEKOSTITDPLWAAVEEUCILGARBEATAVGETAAL
 SIQKQTMQQLSTSGLINTNEERNSTKRTSSEDSYSPRSKHTOSHGLCDISGNHS
 HGUNGEYGSNNMSFYNTSPVAQSLPFLRNFOAVANNSLTDSSPSKTNY
 LQAPRKEDVFDGKLRKIGRFLFSDSPRSRSLADSAGANINSSATVSGNINNASKY
 LGGSKLSSLARSITVLRKGSHAWNEMDGEYRGEEFDDSPNTSATGGMASNDDE
 TMSIGGAMSSQTITGSELLNURLTGBCRLLSYMRYCOEALDTYMKDPKHNTG
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BASE COUNT 558 a 405 c 404 g 548 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.97e-05 Length: 1915
 Score: 91.00 Matches: 18
 Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 75.00% Mismatches: 3
 Query Match: 75.21% Indels: 0
 DB: 8 Gaps: 0

US-10-036-492-6 (1-24) x AY126780 (1-1915)

Qy 1 ValAsnLeuGlnLeuAlaArgCysteTyLeuSerAsnSerGlnAlaTySerAlaTy 20
 Db 106 GTTAATTCGACTTATGCCACCGATTCTGCAGATAATCACGTACAGTGCTAT 165

RESULT: 9

AY126780 LCUS AY126780 1915 bp mRNA linear PLN 07-AUG-2002
 DEFINITION Arabidopsis thaliana CDC27/NCIC2-like protein (At2g20000) mRNA,
 complete cds.
 ACCESSION AY126780
 VERSION AY126780.1 GI:22136203
 KEYWORDS SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana; Streptophytina; Embryophytina; Tracheophytina;
 Eukaryota; Viridiplantae; Magnoliophytina; eudicots; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1915) FLI C DNA.
 AUTHORS Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M.,
 Palm, C.J., Bowser, L., Jones, T., Bath, J., Carninci, P., Chen, H.,

COMMENT 1 ValAsnLeuGlnLeuAlaArgCysteTyLeuSerAsnSerGlnAlaTySerAlaTy 20
 106 GTTAATTCGACTTATGCCACCGATTCTGCAGATAATCACGTACAGTGCTAT 165

COMMENT 21 TyrIleLeuLys 24

COMMENT 21 TyrIleLeuLys 24

TITLE A Plant development regulating gene and its uses
JOURNAL Patent: WO 023859-A 3 16-MAY-2002;
FEATURES Universiteit Utrecht (NL)
source Location/Qualifiers

1. .2235 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

BASE COUNT 664 a -475 c 484 g 612 t
ORIGIN

Alignment Scores:
Pred. No.: 2.326-05 Length: 2235
Score: 91.00 Matches: 18
Percent Similarity: 87.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 3
Query Match: 75.21% Indels: 0
DB: 6 Gaps: 0

US-10-036-492-6 (1-24) x AX462179 (1-2235)

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
Db 106 GTTAATTGGAGCTTATTGCCACCAAGCTACTGTGAGATAATCAGCTTACAGTCATAT 165

QY 21 TyrIleLeuLys 24

Db 166 CATCGCTAAG 177

RESULT 14
LOCUS AX462193 2235 bp DNA linear PAT 09-JUL-2002
DEFINITION Sequence 17 from Patent WO0238599.
ACCESSION AX462193
VERSION AX462193.1 GI:21727752

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyte; Magnoliophyta; eudicots; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

ORGANISM

REFERENCE 1 Scheres, B.J., Blijlevens, I. and Bolmer, S.D.
AUTHORS A Plant development regulating gene and its uses
JOURNAL Patent: WO 023859-A 19 16-MAY-2002;
Universiteit Utrecht (NL)
FEATURES Location/Qualifiers

1. .2235 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

BASE COUNT 665 a -475 c 483 g 612 t
ORIGIN

Alignment Scores:
Pred. No.: 2.326-05 Length: 2235
Score: 91.00 Matches: 18
Percent Similarity: 87.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 3
Query Match: 75.21% Indels: 0
DB: 6 Gaps: 0

US-10-036-492-6 (1-24) x AX462195 (1-2235)

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
Db 106 GTTAATTGGAGCTTATTGCCACCAAGCTACTGTGAGATAATCAGCTTACAGTCATAT 165

QY 21 TyrIleLeuLys 24

Db 166 CATCGCTAAG 177

Search completed: February 2, 2004, 15:40:00
Job time : 6296 secs

FEATURES
source Location/Qualifiers

1. .2235 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

BASE COUNT 664 a -474 c 484 g 613 t
ORIGIN

Alignment Scores:
Pred. No.: 2.326-05 Length: 2235
Score: 91.00 Matches: 18
Percent Similarity: 87.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 3
Query Match: 75.21% Indels: 0
DB: 6 Gaps: 0

US-10-036-492-6 (1-24) x AX462193 (1-2235)

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysTyrLeuSerAsnSerGlnAlaTyrSerAlaTyr 20
Db 106 GTTAATTGGAGCTTATTGCCACCAAGCTACTGTGAGATAATCAGCTTACAGTCATAT 165

QY 21 TyrIleLeuLys 24

Db 166 CATCGCTAAG 177

RESULT 15

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2004, 12:47:18 ; Search time 247 Seconds
(without alignments)
20.193 Million cell updates/sec

Title: US-10-036-492-6

Perfect score: 121

Sequence: 1 VNLQLARCYLSNSQAYSAYILK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters:

789580

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:*

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3: /cgns_6/podata/1/pubpa/us06_pub.pep:*
4: /gnz_6/podata/1/pubpa/us06_pubcomb.pep:*
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9: /cgns_6/podata/1/pubpa/us09_pubcomb.pep:*
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13: /cgns_6/podata/1/pubpa/us10_pubcomb.pep:*
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15: /cgns_6/podata/1/pubpa/us11c_pubcomb.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	24	14	US-10-036-492-6
2	121	100.0	716	14	US-10-036-492-11
3	121	100.0	728	14	US-10-036-492-10
4	91	75.2	161	14	US-10-036-492-13
5	91	75.2	739	14	US-10-036-492-32
6	46	38.0	556	9	US-09-987-586A-32
7	46	38.0	556	11	US-09-903-012-32
8	46	38.0	882	12	US-10-104-047-3543
9	46	38.0	167	12	US-10-191-813-65
10	44.5	36.8	205	12	US-10-191-813-55
11	44.5	36.8	205	12	US-10-191-813-59
12	44.5	36.8	205	12	US-10-191-813-61
13	44.5	36.8	205	12	US-10-191-813-63
14	44.5	36.8	205	12	US-10-191-813-68
15	44.5	36.8	205	12	US-10-191-813-68

| Result No. | Score | Query Match | Length | DB ID | Description |
</tr
| --- | --- | --- | --- | --- | --- |

APPLICANT: HEMERLY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE
 TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 217943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 11
 LENGTH: 716
 ORGANISM: Arabidopsis thaliana
 US-10-036-492-11

Query Match 100.0%; Score 121; DB 14; Length 716;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNQLLARCYLSNSQAYSSAYILK 24
 Db 37 VNQLLARCYLSNSQAYSSAYILK 60

RESULT 3
 US-10-036-492-5

Sequence 5, Application US/10036492
 Publication No. US20020164757A1
 GENERAL INFORMATION
 APPLICANT: HEMERLY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE
 TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 217943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 5
 LENGTH: 728
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-036-492-5

Query Match 100.0%; Score 121; DB 14; Length 728;

Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNQLLARCYLSNSQAYSSAYILK 24
 Db 37 VNQLLARCYLSNSQAYSSAYILK 60

RESULT 4
 US-10-036-492-10

Sequence 10, Application US/10036492
 Publication No. US20020164757A1
 GENERAL INFORMATION
 APPLICANT: HEMERLY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE
 TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 217943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: Patentin version 3.1

Query Match 100.0%; Score 121; DB 14; Length 728;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNQLLARCYLSNSQAYSSAYILK 24
 Db 36 VNQLLATSYLNQNOQAYSAHILK 59

RESULT 5
 US-10-036-492-13

Sequence 13, Application US/10036492
 Publication No. US20020164757A1
 GENERAL INFORMATION
 APPLICANT: HEMERLY, ADRIANA
 APPLICANT: FERREIRA, PAULO
 APPLICANT: ROMBAUTS, STEPHANE
 TITLE OF INVENTION: PLANT DNA REPLICATION MODULATING PROTEINS
 FILE REFERENCE: 217943US0XCONT
 CURRENT APPLICATION NUMBER: US/10/036,492
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: EP 99202214.5
 PRIOR FILING DATE: 1999-07-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 13
 LENGTH: 739
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-036-492-13

Query Match 100.0%; Score 91; DB 14; Length 739;

Best Local Similarity 75.0%; Pred. No. 1.2e-05;
 Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNQLLARCYLSNSQAYSSAYILK 24
 Db 36 VNQLLATSYLNQNOQAYSAHILK 59

RESULT 6
 US-09-887-586A-32

Sequence 32, Application US/09887586A
 Patient No. US2000094556A1
 GENERAL INFORMATION
 APPLICANT: Chappell, Joseph
 APPLICANT: No. US20020094556A1, Joseph P.
 APPLICANT: Starks, Courtney M.
 APPLICANT: Mama, Kathleen R.
 TITLE OF INVENTION: SYNTHASES
 FILE REFERENCE: 07670-025001
 CURRENT APPLICATION NUMBER: US/09/887,586A
 CURRENT FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 09/398,335
 PRIOR FILING DATE: 1999-05-17
 PRIOR APPLICATION NUMBER: 60/130,628
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: 60/150,262
 PRIOR FILING DATE: 1999-08-23
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 32
 LENGTH: 556
 TYPE: PRT
 ORGANISM: Solanum tuberosum

US-09-887-586A-32
 Query Match Score 46; DB 9; Length 556;
 Best Local Similarity 64.3%; Pred. No. 81;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;
 SEQ ID NO: 10 YLSNSQAYSAVYIL 23
 DB 402 YLSNALATSTYLL 415

RESULT 7
 US-09-903-012-32
 Sequence 32, Application US/09903012
 GENERAL INFORMATION:
 APPLICANT: Chappell, Joseph P.
 APPLICANT: Starks, Courtney M.
 APPLICANT: Mann, Kathleen R.
 TITLE OF INVENTION: SYNTHASES
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/903, 012
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: 09/398, 395
 PRIOR FILING DATE: 1999-01-17
 PRIOR APPLICATION NUMBER: 60/100, 993
 PRIOR FILING DATE: 1999-09-18
 PRIOR APPLICATION NUMBER: 60/130, 628
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: 60/150, 262
 PRIOR FILING DATE: 1999-08-23
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 32
 LENGTH: 556
 TYPE: PRT
 ORGANISM: Solanum tuberosum
 US-09-903-012-32

Query Match Score 46; DB 9; Length 556;
 Best Local Similarity 64.3%; Pred. No. 81;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;
 SEQ ID NO: 10 YLSNSQAYSAVYIL 23
 DB 402 YLSNALATSTYLL 415

RESULT 8
 US-09-900-797-32
 Sequence 32, Application US/09900797
 GENERAL INFORMATION:
 APPLICANT: Chappell, Joseph P.
 APPLICANT: No. US20030087406A1, Joseph P.
 APPLICANT: Starks, Courtney M.
 APPLICANT: Mann, Kathleen R.
 TITLE OF INVENTION: SYNTHASES
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/900, 797
 CURRENT FILING DATE: 2001-07-06
 PRIOR APPLICATION NUMBER: US/09/398, 395
 PRIOR FILING DATE: 1999-09-17
 PRIOR APPLICATION NUMBER: 60/130, 628
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: 60/150, 262
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 32
 LENGTH: 556
 TYPE: PRT

RESULT 9
 US-10-104-047-3543
 Sequence 354, Application US/10104047
 Publication No. US20030236392A1
 GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: No. US003236392A1 full length cDNA
 FILE REFERENCE: HI-A0105
 CURRENT APPLICATION NUMBER: US/10/104, 047
 CURRENT FILING DATE: 2002-03-25
 PRIOR APPLICATION NUMBER:
 PRIOR FILING DATE:
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 3543
 LENGTH: 882
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-104-047-3543

Query Match Score 46%; DB 12; Length 882;
 Best Local Similarity 50.0%; Pred. No. 1.3e-02;
 Matches 9; Conservative 1; Mismatches 8; Indels 0;
 Gaps 0;

RESULT 10
 US-10-191-813-65
 Sequence 65, Application US/10191813
 Publication No. US2003165907A1
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 APPLICANT: Burgess, Loyd R.
 APPLICANT: Brunnen, Kurt R.
 TITLE OF INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/10/191, 813
 CURRENT FILING DATE: 2003-07-09
 PRIOR APPLICATION NUMBER: US/09/191, 468
 PRIOR FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SEQ ID NO: 65
 LENGTH: 167
 TYPE: PRT
 ORGANISM: Human
 US-10-191-813-65

Query Match Score 44.5%; DB 12; Length 167;
 Best Local Similarity 40.0%; Pred. No. 38;
 Matches 10; Conservative 6; Mismatches 8; Indels 1;
 Gaps 1;

RESULT 11
 US-131-VNFTSLANKTFSSEEYFKFVK 155

US-10-191-813-55
*/ Sequence 55, Application US/10191813
 / Publication No. US20030165907A1
 / GENERAL INFORMATION:
 / APPLICANT: Gallagher, Michael J.
 / APPLICANT: Burgess, Loyd R.
 / APPLICANT: Brunden, Kurt R.
 / TITLE OF INVENTION: Human Glycine Transporter Type 2
 / FILE REFERENCE: 123111US01
 / CURRENT APPLICATION NUMBER: US/10/191,813
 / CURRENT FILING DATE: 2002-07-09
 / PRIOR APPLICATION NUMBER: US/09/191,468
 / PRIOR FILING DATE: 1998-11-12
 / NUMBER OF SEQ ID NOS: 124
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 55
 / LENGTH: 205
 / TYPE: PRT
 / ORGANISM: Human
 US-10-191-813-55*

Query Match 36.8%; Score 44.5%; DB 12; Length 205;
 Best Local Similarity 40.0%; Pred. No. 47;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 VNQLLA-RCYLSNSQAYSAVILK 24
 Db 131 VNFTSLANKTFVSGSEEFKYFVLK 155

RESULT 14
 US-10-191-813-63
*/ Sequence 63, Application US/10191813
 / Publication No. US20030165907A1
 / GENERAL INFORMATION:
 / APPLICANT: Gallagher, Michael J.
 / APPLICANT: Burgess, Loyd R.
 / APPLICANT: Brunden, Kurt R.
 / TITLE OF INVENTION: Human Glycine Transporter Type 2
 / FILE REFERENCE: 123111US01
 / CURRENT APPLICATION NUMBER: US/10/191,813
 / CURRENT FILING DATE: 2002-07-09
 / PRIOR APPLICATION NUMBER: US/09/191,468
 / PRIOR FILING DATE: 1998-11-12
 / NUMBER OF SEQ ID NOS: 124
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 63
 / LENGTH: 205
 / TYPE: PRT
 / ORGANISM: Human
 US-10-191-813-63*

Query Match 36.8%; Score 44.5%; DB 12; Length 205;
 Best Local Similarity 40.0%; Pred. No. 47;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 VNQLLA-RCYLSNSQAYSAVILK 24
 Db 131 VNFTSLANKTFVSGSEEFKYFVLK 155

RESULT 15
 US-10-191-813-68
*/ Sequence 68, Application US/10191813
 / Publication No. US20030165907A1
 / GENERAL INFORMATION:
 / APPLICANT: Gallagher, Michael J.
 / APPLICANT: Burgess, Loyd R.
 / APPLICANT: Brunden, Kurt R.
 / TITLE OF INVENTION: Human Glycine Transporter Type 2
 / FILE REFERENCE: 123111US01
 / CURRENT APPLICATION NUMBER: US/10/191,813
 / CURRENT FILING DATE: 2002-07-09
 / PRIOR APPLICATION NUMBER: US/09/191,468
 / PRIOR FILING DATE: 1998-11-12
 / NUMBER OF SEQ ID NOS: 124
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 68
 / LENGTH: 205
 / TYPE: PRT
 / ORGANISM: Human
 US-10-191-813-68*

Query Match 36.8%; Score 44.5%; DB 12; Length 205;

US-10-191-813-61
*/ Sequence 61, Application US/10191813
 / Publication No. US20030165907A1
 / GENERAL INFORMATION:
 / APPLICANT: Gallagher, Michael J.
 / APPLICANT: Burgess, Loyd R.
 / APPLICANT: Brunden, Kurt R.
 / TITLE OF INVENTION: Human Glycine Transporter Type 2
 / FILE REFERENCE: 123111US01
 / CURRENT APPLICATION NUMBER: US/10/191,813
 / CURRENT FILING DATE: 2002-07-09*

Query Match 36.8%; Score 44.5%; DB 12; Length 205;

Tue Feb 3 10:50:16 2004

us-10-036-492-6.rapb

Page 5

Best Local Similarity 40.0%; Pred. No. 47;
Matches 10; Conservative 6; Mismatches 8;
Indels 1; Gaps 1;

Qy 1 VNLOQLA-RCYLSNSQAYAYIILK 24
| | : | : | : | : | : |
Db 131 VNFTSLANKTFVSGSEEYFKYFVLK 155

Search completed: February 2, 2004, 13:25:00
Job time : 247 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2004, 12:50:28 ; Search time 76 seconds
 (without alignments)
 13.361 Million cell updates/sec

Title: US-10-036-492-6

Perfect score: 121

Sequence: 1 VNLQLARCVLSQASAYVILK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 322717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents AA:*

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2: /cgtn2_6/ptodata/1/iaa/5a_COMB.pep:*

3: /cgtn2_6/ptodata/1/iaa/6a_COMB.pep:*

4: /cgtn2_6/ptodata/1/iaa/6b_COMB.pep:*

5: /cgtn2_6/ptodata/1/iaa/6b_POTUS_COMB.pep:*

6: /cgtn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	38.0	213	4 US-09-134-001C-5360	Sequence 5360, AP
2	46	38.0	556	4 US-09-398-195A-32	Sequence 32, App1
3	46	38.0	556	4 US-09-887-586A-32	Sequence 32, App1
4	46	38.0	556	4 US-09-955-1522-32	Sequence 32, App1
5	46	38.0	556	4 US-09-903-012B-32	Sequence 32, App1
6	46.8	167	4	US-09-191-468-65	Sequence 65, App1
7	44.5	36.8	205	4 US-09-191-468-55	Sequence 55, App1
8	44.5	36.8	205	4 US-09-191-468-59	Sequence 59, App1
9	44.5	36.8	205	4 US-09-191-468-61	Sequence 61, App1
10	44.5	36.8	205	4 US-09-191-468-63	Sequence 63, App1
11	44.5	36.8	205	4 US-09-191-468-68	Sequence 68, App1
12	44.5	36.8	205	4 US-09-191-468-70	Sequence 70, App1
13	44.5	36.8	797	4 US-09-191-468-120	Sequence 120, App
14	44.5	36.8	797	4 US-09-191-468-122	Sequence 122, App
15	44.5	36.8	831	2 US-09-047-026A-4	Sequence 4, App1
16	44	36.4	308	4 US-09-252-991A-28210	Sequence 28210, A
17	43	35.5	299	2 US-09-047-026A-24	Sequence 24, App1
18	42	34.7	634	4 US-09-328-1522-627	Sequence 4627, Ap
19	41	33.9	150	4 US-09-107-532A-512B	Sequence 512B, Ap
20	41	33.9	161	4 US-09-107-532A-186	Sequence 7186, Ap
21	40	33.1	205	4 US-09-191-468-57	Sequence 57, App1
22	40	33.1	354	2 US-09-701-013B-9	Sequence 9, App1
23	40	33.1	405	2 US-08-701-013B-6	Sequence 6, App1
24	40	33.1	434	2 US-08-484-75A-20	Sequence 20, App1
25	40	33.1	434	3 US-08-477-59-20	Sequence 20, App1
26	40	33.1	434	3 US-08-479-56-20	Sequence 20, App1
27	40	33.1	434	3 US-08-486-414-46	Sequence 46, App1

ALIGNMENTS

28	40	33.1	434	5 PCT-US94-01826A-20	Sequence 20, App1
29	40	33.1	434	5 PCT-US94-02252A-20	Sequence 20, App1
30	40	33.1	434	5 PCT-US96-03916-11	Sequence 67, App1
31	40	33.1	434	5 PCT-US96-03916-67	Sequence 67, App1
32	40	33.1	548	4 US-09-398-195A-2	Sequence 2, App1
33	40	33.1	548	4 US-09-198-195A-4	Sequence 6, App1
34	40	33.1	548	4 US-09-398-195A-6	Sequence 8, App1
35	40	33.1	548	4 US-09-398-195A-8	Sequence 10, App1
36	40	33.1	548	4 US-09-398-195A-10	Sequence 12, App1
37	40	33.1	548	4 US-09-887-586A-2	Sequence 4, App1
38	40	33.1	548	4 US-09-887-586A-4	Sequence 6, App1
39	40	33.1	548	4 US-09-887-586A-6	Sequence 8, App1
40	40	33.1	548	4 US-09-887-586A-8	Sequence 10, App1
41	40	33.1	548	4 US-09-887-586A-10	Sequence 2, App1
42	40	33.1	548	4 US-09-895-752-2	Sequence 4, App1
43	40	33.1	548	4 US-09-895-752-4	Sequence 6, App1
44	40	33.1	548	4 US-09-895-752-6	Sequence 8, App1
45	40	33.1	548	4 US-09-895-752-8	Sequence 10, App1

NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 32
 LENGTH: 556
 TYPE: PRT
 ORGANISM: Solanum tuberosum
 US-09-398-35A-32

Query Match 38.0%; Score 46; DB 4; Length 556;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 10 YLSNSQAYSAYYL 23
 Db 402 YLSNALATSTYLL 415

RESULT 3
 US-09-887-586A-32
 / Sequence 32, Application US/09887586A
 / Patent No. 6493354
 / GENERAL INFORMATION:
 / APPLICANT: Chappell, Joseph
 / APPLICANT: Starks, Courtney M.
 / APPLICANT: Manna, Kathleen R.
 / TITLE OF INVENTION: SYNTHASES
 / FILE REFERENCE: 07678-025001
 / CURRENT APPLICATION NUMBER: US/09/887_586A
 / CURRENT FILING DATE: 2001-06-22
 / PRIOR APPLICATION NUMBER: 09/398_395
 / PRIOR FILING DATE: 1999-09-17
 / PRIOR APPLICATION NUMBER: 60/130_628
 / PRIOR FILING DATE: 1999-04-22
 / PRIOR APPLICATION NUMBER: 60/150_262
 / PRIOR FILING DATE: 1999-08-23
 / NUMBER OF SEQ ID NOS: 58
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 32
 / LENGTH: 556
 / TYPE: PRT
 / ORGANISM: Solanum tuberosum
 US-09-887-586A-32

Query Match 38.0%; Score 46; DB 4; Length 556;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 10 YLSNSQAYSAYYL 23
 Db 402 YLSNALATSTYLL 415

RESULT 4
 US-09-895-752-32
 / Sequence 32, Application US/09895752
 / Patent No. 6559297
 / GENERAL INFORMATION:
 / APPLICANT: Chappell, Joseph
 / APPLICANT: Starks, Courtney M.
 / APPLICANT: Manna, Kathleen R.
 / TITLE OF INVENTION: SYNTHASES
 / FILE REFERENCE: 07678-025001
 / CURRENT APPLICATION NUMBER: US/09/895_752
 / CURRENT FILING DATE: 2001-06-29
 / PRIOR APPLICATION NUMBER: 09/398_395
 / PRIOR FILING DATE: 1999-09-17
 / PRIOR APPLICATION NUMBER: 60/100_993
 / PRIOR FILING DATE: 1999-09-18
 / PRIOR APPLICATION NUMBER: 60/150_262
 / PRIOR FILING DATE: 1999-08-23
 / NUMBER OF SEQ ID NOS: 58
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 32
 / LENGTH: 556
 / TYPE: PRT
 / ORGANISM: Solanum tuberosum
 US-09-895-752-32

Query Match 38.0%; Score 46; DB 4; Length 556;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 10 YLSNSQAYSAYYL 23
 Db 402 YLSNALATSTYLL 415

RESULT 5
 US-09-903-012B-32
 / Sequence 32, Application US/09903012B
 / Patent No. 6569356
 / GENERAL INFORMATION:
 / APPLICANT: Chappell, Joseph P.
 / APPLICANT: No. 65616561, Joseph P.
 / APPLICANT: Starks, Courtney M.
 / APPLICANT: Manna, Kathleen R.
 / TITLE OF INVENTION: SYNTHASES
 / FILE REFERENCE: 07678-025001
 / CURRENT APPLICATION NUMBER: US/09/903_012B
 / CURRENT FILING DATE: 2001-07-11
 / PRIOR APPLICATION NUMBER: 60/100_993
 / PRIOR FILING DATE: 1998-09-18
 / PRIOR APPLICATION NUMBER: 60/130_628
 / PRIOR FILING DATE: 1999-04-22
 / PRIOR APPLICATION NUMBER: 60/150_262
 / PRIOR FILING DATE: 1999-08-23
 / NUMBER OF SEQ ID NOS: 58
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 32
 / LENGTH: 556
 / TYPE: PRT
 / ORGANISM: Solanum tuberosum
 US-09-903-012B-32

Query Match 38.0%; Score 46; DB 4; Length 556;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 3; Indels 0;
 Gaps 0;

Qy 10 YLSNSQAYSAYYL 23
 Db 402 YLSNALATSTYLL 415

RESULT 6
 US-09-191-468-65
 / Sequence 65, Application US/09191468A
 / Patent No. 6416915
 / GENERAL INFORMATION:
 / APPLICANT: Gallagher, Michael J.
 / APPLICANT: Burgess, Loyd R.
 / APPLICANT: Brunden, Kurt R.
 / TITLE OF INVENTION: Human Glycine Transporter Type 2
 / FILE REFERENCE: 12311US01
 / CURRENT APPLICATION NUMBER: US/09/191_468A
 / CURRENT FILING DATE: 1998-11-12
 / NUMBER OF SEQ ID NOS: 124
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 65
 / LENGTH: 167
 / TYPE: PRT
 / ORGANISM: Human
 US-09-191-468-65

Query Match 36.8%; Score 44.5%; DB 4; Length 167;
 Best Local Similarity 40.0%; Pred. No. 8.4;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 VNQLQIA-RCYLSNSQAYSAVYILK 24
 Db 131 VNFTSLANKTFVSGSEEYFKYFVLK 155

RESULT 7
 US-09-191-468-55
 Sequence 55, Application US/09191468A
 Patent No. 6416975
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 ATTORNEY: Burgess, Loyd R.
 INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 55
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-55

Query Match 36.8%; Score 44.5%; DB 4; Length 205;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 VNQLQIA-RCYLSNSQAYSAVYILK 24
 Db 131 VNFTSLANKTFVSGSEEYFKYFVLK 155

RESULT 8
 US-09-191-468-59
 Sequence 59, Application US/09191468A
 Patent No. 6416975
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 ATTORNEY: Burgess, Loyd R.
 INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 59
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-59

Query Match 36.8%; Score 44.5%; DB 4; Length 205;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 VNQLQIA-RCYLSNSQAYSAVYILK 24
 Db 131 VNFTSLANKTFVSGSEEYFKYFVLK 155

RESULT 9
 US-09-191-468-61
 Sequence 61, Application US/09191468A
 Patent No. 6416975
 GENERAL INFORMATION:

Query Match 36.8%; Score 44.5; DB 4; Length 205;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
 SEQ ID NO: 131 VNFSLANKTPVSGSEEFKVFVLK 155

RESULT 12
 US-09-191-468-70
 Sequence 70, Application US/09191468A
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 APPLICANT: Burgess, Loyd R.
 APPLICANT: Brunden, Kurt R.
 TITLE OF INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 70
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-70
 Sequence 120, Application US/09191468A
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 APPLICANT: Burgess, Loyd R.
 APPLICANT: Brunden, Kurt R.
 TITLE OF INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 70
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-70
 Sequence 120, Application US/09191468A
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 APPLICANT: Burgess, Loyd R.
 APPLICANT: Brunden, Kurt R.
 TITLE OF INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 120
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-120
 Sequence 120, Application US/09191468A
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.
 APPLICANT: Burgess, Loyd R.
 APPLICANT: Brunden, Kurt R.
 TITLE OF INVENTION: Human Glycine Transporter Type 2
 FILE REFERENCE: 12311US01
 CURRENT APPLICATION NUMBER: US/09/191,468A
 CURRENT FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 120
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Human
 US-09-191-468-120
 Sequence 120, Application US/09191468A
 GENERAL INFORMATION:
 APPLICANT: Gallagher, Michael J.

; APPLICANT: Burgess, Loyd R.
; APPLICANT: Brunden, Kurt R.
; TITLE OF INVENTION: Human Glycine Transporter Type 2
; FILE REFERENCE: 12311US01
; CURRENT APPLICATION NUMBER: US/09/191,468A
; CURRENT FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 122
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Human
; US-09-191-468-122
; Query Match 36.9%; Score 44.5; DB 4; Length 797;
; Best Local Similarity 40.0%; Pred. No. 56;
; Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
; SEQ ID NO: 131 VNLQLLA-RCYLSNSQAYSAYILK 24
; 357 VNFTSLANKTPVSGSEEFKVFVLK 381
; RESULT 15
; US-09-047-026A-4
; Sequence 4, Application US/09047026A
; Patent No. 5989897
; GENERAL INFORMATION:
; APPLICANT: Pillus, Lorraine
; APPLICANT: Clarke, Astrid
; APPLICANT: Lowell, Joanna
; APPLICANT: Jacobson, Sandra
; APPLICANT: Reifsnnyder, Cheryl
; TITLE OF INVENTION: Yeast Silencing Genes, Proteins and
; Methods
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winer and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,026A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,375
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 1-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 amino acids
; TYPE: amino
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-047-026A-4
; Query Match 36.8%; Score 44.5; DB 2; Length 831;
; Best Local Similarity 37.0%; Pred. No. 59;
; Matches 10; Conservative 6; Mismatches 6; Indels 5; Gaps 1;
; SEQ ID NO: 131 VNLQLLA-RCYLSNSQAYSAYILK 24
; 357 VNFTSLANKTPVSGSEEFKVFVLK 381
; RESULT 14
; US-09-191-468-122
; Sequence 122, Application US/09191468A
; Patent No. 6416915
; GENERAL INFORMATION:
; APPLICANT: Gallagher, Michael J.

QY 2 NLQLARCYLSNSQAY----SAYYL 23
| | | | : . . . : | |
Db 355 NLCILAKCFINSKLYDVEPFFIYIL 381

Search completed: February 2, 2004, 13:26:27
Job time : 76 secs

KW Cell cycle regulation; DNA replication; CDC7; CDC27A1; CDC27A2;
 KW CDC27B; nematode resistance; endoreduplication; sterility;
 KW polyploidy.
 XX

OS Arabidopsis thaliana.

XX WO200102430-A2.

XX 11-JAN-2001.

PD 05-JUL-2000; 2000WO-EPO6401.

XX 05-JUL-1999; 98EP-0202214.

XX (CROP-) CROPDFSIGN NV.

PA (UYRI-) UNIV RIO DE JANEIRO.

XX Hemerly AS, Ferreira PCG, Rombauts S;

PI DR; 2001-123101/13.

XX PR Partially purified plant CDC27 or CDC7 protein homolog, useful for modulating DNA replication and for producing transgenic plants -

PS Claim 1; Page 6; 86pp; English.

XX The present invention provides the protein and coding sequences of several Arabidopsis thaliana proteins which are involved in DNA

replication and the regulation of the cell cycle. These include CDC7,

CDC27A1, CDC27A2 and CDC27B. They are useful in the production of

transgenic and mutant plants, as the mutations in the gene cause

proteins to confer nematode resistance, sterility and polyploidy on

plants and also lead to endoreduplication.

CC Note: This sequence is stated as being the same as that given as SEQ ID

NO: 6 in the sequence listing of the specification. However, this

CC sequence is longer than that shown here.

XX sequence 23 AA;

XX Query Match 88.0%; Score 106.5; DB 22; Length 23;

XX Best Local Similarity 95.8%; Prod. No. 1.1e-03; Indels 0; Gaps 1;

XX Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

XX Qy 1 VNQLQLLARCYLSNSQAYSAVYILK 24

XX Db 1 VNQLQLLARCYLSN-QAYSAVYILK 23

XX

XX RESULT 5

XX ABB68955

XX ID AAB68955 standard; peptide: 161 AA.

XX AC AAB68955;

XX XX 18-APR-2001 (first entry)

XX Arabidopsis thaliana CDC27B protein fragment.

XX Cell cycle regulation; DNA replication; CDC7; CDC27A1; CDC27A2;

KW KW CDC27B; nematode resistance; endoreduplication; sterility;

KW polyploidy.

XX OS Arabidopsis thaliana.

XX PN WO200102430-A2.

XX PD 11-JAN-2001.

XX 05-JUL-2000; 2000WO-EPO6401.

XX PR 05-JUL-1999; 98EP-0202214.

XX (CROP-) CROPDFSIGN NV.

PA

PA (UYRI-) UNIV RIO DE JANEIRO.

XX Hemerly AS, Ferreira PCG, Rombauts S;

XX WPI; 2001-123101/13.

XX PR Partially purified Plant CDC27 or CDC7 protein homolog, useful for modulating DNA replication and for producing transgenic plants -

XX PT Claim 1; Page 78; 86pp; English.

XX

The present invention provides the protein and coding sequences of

several Arabidopsis thaliana proteins which are involved in DNA

replication and the regulation of the cell cycle. These include CDC7,

CDC27A1, CDC27A2 and CDC27B. They are useful in the production of

transgenic and mutant plants, as the mutations in the gene cause

proteins to confer nematode resistance, sterility and polyploidy on

plants and also lead to endoreduplication.

XX

XX Sequence 161 AA;

XX Query Match 75.2%; Score 91; DB 22; Length 161;

XX Best Local Similarity 75.0%; Prod. No. 2.7e-06;

XX Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

XX SQ Sequence 161 AA;

XX Query Match 75.2%; Score 91; DB 22; Length 161;

XX Best Local Similarity 75.0%; Prod. No. 2.7e-06;

XX Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

XX SQ Sequence 161 AA;

XX Query Match 1 VNQLQLLARCYLSNSQAYSAVYILK 24

XX Db 36 VNQLQLLARCYLSNSQAYSAVYILK 59

XX

XX RESULT 6

XX ABGG65520

XX ID ABGG65520 standard; Protein; 162 AA.

XX AC ABGG65520;

XX DT 23-AUG-2002 (first entry)

XX XX Cell cycle regulation protein HOBBIT (HBT) #1.

XX XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; Plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry.

XX XX OS Arabidopsis thaliana.

XX XX PN WO200238559-A2.

XX XX 16-MAY-2002.

XX XX WO200238559-A2.

XX XX 16-MAY-2002.

XX XX FF 13-NOV-2001; 2001WO-EPI3116.

XX XX PR 13-NOV-2000; 2000EP-0810271.

XX XX PR 30-NOV-2000; 2000US-250402P.

XX XX PA (UYRI-) RIJKSUNIV UTRECHT.

XX XX PI Scheres BJG, Blilou I, Polymer SDH;

XX XX DR WPI; 2002-490065/52.

XX XX N-PSDB; ABK93343.

XX XX PR Use of plant cdc27B for modulating or mimicking auxin-related effects in plants or plant cells, or for regulation of cell cycle of plant cell

XX XX PS Claim 30; Page 144-145; 207BP; English.

XX XX CC The inventon described the use of a plant cdc27B (also termed HOBBIT

(HBT) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or modification of the arrangement of organs and/or tissues in a plant; increased plant yield; an increased survival rate of plants; an enhanced survival rate under drought conditions; increase of seedling emergency; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and Proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or Plant biochemistry. This is the amino acid sequence of an *Arabidopsis thaliana* HOBBIT (HBT) or cdc27B protein described in the invention.

XX Sequence 162 AA;

Query Match 75.2%; Score 91; DB 23; Length 162;

Best Local Similarity 75.0%; Pred. No. 2.7e-06; Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNLQLLARCYLSNSQASAYHLK 24

Db 36 VNLQLLATSYLNQNQASAYHLK 59

RESULT 7

ID ABG65521 standard; Protein; 166 AA.

XX AC ABG65521;

XX DT 23-AUG-2002 (first entry)

XX DE Cell cycle regulation protein HOBBIT (HBT) #2.

XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergency; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry.

XX Arabidopsis thaliana.

XX OS WO200238599-A2.

XX PN 13-NOV-2000; 2000USP-0810271.

XX PD 16-MAY-2002.

XX PPA 13-NOV-2001; 2001WO-EP13116.

XX PI RIJKSUNIV Utrecht.

XX WPI 2002-490065/52.

N-PSDB; ABK93344.

XX Use of Plant cdc27B for modulating or mimicking auxin-related effects in Plants or plant cells, or for regulation of cell cycle of plant cell

PR PT PR PR

PS Claim 30; Page 145; 207pp; English.

XX The invention described the use of a Plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in altered cell fate and/or altered pattern formation in a plant or Plant cell; alteration in the size and/or number of naturally occurring Plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased survival rate under drought conditions; increase of seedling emergency; mimicking of root generation in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and Proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or Plant biochemistry. This is the amino acid sequence of an *Arabidopsis thaliana* HOBBIT (HBT) or cdc27B Protein described in the invention.

XX Sequence 166 AA;

Query Match 75.2%; Score 91; DB 23; Length 166;

Best Local Similarity 75.0%; Pred. No. 2.8e-06; Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNLLQLLARCYLSNSQASAYHLK 24

Db 36 VNLLQLLATSYLNQNQASAYHLK 59

RESULT 8

ID ABG65529

ID ABG65529 standard; Protein; 518 AA.

XX AC ABG65529;

XX DT 23-AUG-2002 (first entry)

XX DE Functionally inactive HOBBIT (HBT) protein #6.

XX Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergency; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; plant physiology; plant biochemistry.

XX OS Arabidopsis thaliana.

XX PN WO200238599-A2.

XX PD 16-MAY-2002.

XX PPA 13-NOV-2001; 2001WO-EP13116.

XX PI RIJKSUNIV Utrecht.

XX WO200238599-A2.

XX PN WO200238599-A2.

XX PD 16-MAY-2002.

XX PPA 13-NOV-2001; 2001WO-EP13116.

XX	Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate; pattern formation; plant meristem development; plant yield; drought; seedling emergence; root generation; shade avoidance response; vascular strand formation; patterning; parthenocarpic fruit; cell cycle regulation; endoreduplication; cell division; transgenic plant; plant development; plant morphology; Plant physiology; plant biochemistry.
XX	Arabidopsis thaliana.
XX	WO200238599-A2.
XX	16-MAY-2002..
XX	13-NOV-2001; 2001WO-EPP13116.
XX	13-NOV-2000; 2000EP-0870271.
XX	30-NOV-2000; 2000US-250402P.
XX	(UTUT-) RIJKSUNIV Utrecht.
PA	Scheres BJJG, Blilou I, Folmer SDE;
XX	WPI; 2002-490065/52.
XX	Use of plant cdc27B for modulating or mimicking auxin-related effects in plants or plant cells, or for regulation of cell cycle of plant cell -
XX	Claim 36; Page 188-191; 207pp; English.
XX	The invention described the use of a plant cdc27B (also termed HOBBIT (HBT)) useful for modulating or mimicking auxin-related effects in a plant or plant cell. The modulation or mimicking of auxin-related effects results in: altered cell fate and/or altered pattern formation in a plant or plant cell; alteration in the size and/or number of naturally occurring plant meristems; modification of the numbers of organs or tissues, and/or a modification of the rate of organ or tissue emanation from a plant meristem, and/or a modification of the arrangement of organs and/or tissues in a plant; increased plant yield; an increased survival rate of plants; an enhanced survival rate under drought conditions; increase of seedling emergence; mimicking of root regeneration in tissue cultures; an increased shade avoidance response; altering vascular strand formation and patterning in a plant; or production of parthenocarpic fruits. HBT also regulates the cell cycle of the plant cell results in: modulated endoreduplication in a plant; modulation of sterility in plants; increasing the cell cycle or increase of the rate of cell division; alteration in the size of naturally occurring meristems; a modification in a number of organs or tissues, and/or the modification of the rate of organ or tissue emanation from a plant meristem and/or modification of the arrangement of the organs and/or tissues in a plant and/or an increased plant yield or enhancement of survival rate of plants. A nucleic acid encoding HBT is useful for producing transgenic plants, plant cells or plant tissues and in the regeneration of a plant from a plant cell. HBT nucleic acids and proteins are useful for modifying cell fate, pattern formation, plant development, plant morphology, plant physiology and/or plant biochemistry. This is the amino acid sequence of a functionally inactive Arabidopsis thaliana HOBBIT (HBT) or cdc27B protein described in the invention.
XX	Sequence 722 AA;
SQ	Query Match 75.2%; Score 91; DB 23; Length 722; Best Local Similarity 75.0%; Pred. No. 1.5e-05; Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 1
Db	1 VNQLLARCYLSNSQYSAYTLLK 24 36 VNQLLATTSQNQAYSAYHLIK 59

AAB68958	ID	AAB68958	standard; peptide;	739 AA.
XX	XX	Arabidopsis thaliana	CDC27B protein	
AC	XX	Cell cycle regulation; DNA replication; endoreduplication; nematode resistance; endoreduplication; polyploidy.		
XX	DT	18-APR-2001	(first entry)	
XX	XX	Arabidopsis thaliana	CDC27B protein	
DE	XX	Cell cycle regulation; DNA replication; endoreduplication; nematode resistance; endoreduplication; polyploidy.		
XX	KW	CDC27B; nematode resistance; endoreduplication; polyploidy.		
KW	KW	Cell cycle regulation; DNA replication; endoreduplication; nematode resistance; endoreduplication; polyploidy.		
KW	KW	Cell cycle regulation; DNA replication; endoreduplication; nematode resistance; endoreduplication; polyploidy.		
XX	OS	Arabidopsis thaliana.		
XX	XX	Arabidopsis thaliana.		
PN	XX	WO200102430-A2.		
PD	XX	11-JAN-2001.		
PF	XX	05-JUL-2000; 2000WO-EP06401.		
PR	XX	05-JUL-1999; 99EP-0202214.		
XX	PA	(CROP-) CROPDESIGN NV.		
PA	PA	(YTRI-) UNIV RIO DE JANEIRO.		
XX	PI	Hemerly AS, Ferreira PCG, Rombaut		
XX	DR	WPI; 2001-123101/13.		
PT	XX	Partially purified plant CDC27 or C modulating DNA replication and for		
PT	XX	Claim 3; Page 82-84; 86PP; English.		
PS	XX	The present invention provides the several <i>Arabidopsis thaliana</i> proteins replication and the regulation of the <i>cdc27A1</i> , <i>cdc27A2</i> and <i>CDC27B</i> . They are transgenic and mutant plants, as the proteins to confer nematode resistance plants and also lead to endoreduplication.		
SQ	XX	Sequence 739 AA;		
		Query Match 75.2%; Score		
		Best Local Similarity 75.0%; Pred.		
		Matches 18; Conservative 3; Miss		
Qy	1	VNLQLLARCYLSNSQSYASAYILK 2		
Db	36	VNLQLLATSYLQNQQASYASAYILK 5		
RESULT-12	XX			
ABG65522	ID	ABG65522	standard; Protein;	740 AA.
XX	XX	Plant; cdc27B; cyclin; HOBBIT; HBT;		
AC	XX	pattern formation; plant meristem development; seedling emergence; root generation; vascular strand formation; patterned cell cycle regulation; endoreduplication; transgenic plant; plant development; plant biochemistry.		
XX	DT	23-AUG-2002	(first entry)	
XX	DE	Cell cycle regulation protein HOBBIT		
XX	XX	Plant; cdc27B; cyclin; HOBBIT; HBT;		
KW	KW	pattern formation; plant meristem development; seedling emergence; root generation; vascular strand formation; patterned cell cycle regulation; endoreduplication; transgenic plant; plant development; plant biochemistry.		
KW	KW	Cell cycle regulation protein HOBBIT		

XX pattern formation; plant meristem development; plant yield; drought;
 PW seedling emergence; root generation; shade avoidance response;
 XX vascular strand formation; patterning; parthenocarpic fruit;
 PD cell cycle regulation; endoreduplication; cell division;
 XX transgenic plant; plant development; plant morphology; plant physiology;
 PF plant biochemistry.
 XX
 PR Arabidopsis thaliana.
 OS
 PN WO200238599-A2.
 XX
 DR 16-MAY-2002.
 XX
 PF 13-NOV-2001; 2001WO-EPI13116.
 XX
 PR 13-NOV-2000; 2000EP-0870271.
 XX
 PR 30-NOV-2000; 2000US-250402P.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 XX
 PI Scheres BJJ, Blilou I, Polymer SDH;
 XX
 PS Claim 30; Page 146-149; 207pp; English.
 XX
 DR WPI; 2002-49005/52.
 XX
 PR use of plant cdc27B for modulating or mimicking auxin-related effects
 PT in plants or plant cells, or for regulation of cell cycle of plant cell
 PR -
 XX
 PS Claim 30; Page 146-149; 207pp; English.
 XX
 CC The invention described the use of a plant cdc27B (also termed HOBBIT
 CC) useful for modulating or mimicking auxin-related effects in a
 CC plant or plant cell. The modulation or mimicking of auxin-related effects
 CC results in: altered cell fate and/or altered pattern formation in a plant
 CC or plant cell; alteration in the size and/or number of naturally
 CC occurring plant meristems; modification of the numbers of organs or
 CC tissues; and/or a modification of the rate of organ or tissue emanation
 CC from a plant meristem, and/or a modification of the arrangement of organs
 CC and/or tissues in a plant; increased survival
 CC rate of plants; an enhanced survival rate under drought conditions
 CC increase of seedling emergence; mimicking of root generation in tissue
 CC cultures; an increased shade avoidance response; altering vascular strand
 CC formation and patterning in a plant; or production of parthenocarpic
 CC fruits. HOBBIT also regulates the cell cycle of the plant cell results in:
 CC modulated endoreduplication in a plant; modulation of sterility in
 CC plants; increasing the cell cycle or increase of the rate of cell
 CC division; alteration in the size of naturally occurring meristems; a
 CC modification in a number of organs or tissues; and/or the modification of
 CC the rate of organ or tissue emanation from a plant meristem and/or
 CC modification of the arrangement of the organs and/or tissues in a plant
 CC and/or an increased plant yield or enhancement of survival rate of
 CC plants. A nucleic acid encoding HOBBIT is useful for producing transgenic
 CC plants, plant cells or plant tissues and in the regeneration of a plant
 CC morphology, plant physiology and/or plant biochemistry. This is the amino
 CC sequence in the invention.
 XX
 SQ Sequence 740 AA;
 CC Query Match 75.2%; Score 91; DB 23; Length 743;
 CC Best Local Similarity 75.0%; Pred. No. 1.6e-05;
 CC Matches 18; Conservative 3; N mismatches 3; Indels 0; Gaps 0;
 CC
 CC Qy 1 VNLQLIARCLNSNSQAYSAVILK 24
 CC 36 VNLQLIARCLNSNSQAYSAVILK 59
 CC
 DB Sequence 743 AA;
 CC Query Match 75.2%; Score 91; DB 23; Length 743;
 CC Best Local Similarity 75.0%; Pred. No. 1.6e-05;
 CC Matches 18; Conservative 3; N mismatches 3; Indels 0; Gaps 0;
 CC
 CC RESULT 13
 ID ABG65524 standard; Protein; 743 AA.
 XX
 AC ABG65524;
 XX
 DT 23-AUG-2002 (first entry)
 XX
 DE Functionally inactive HOBBIT (HBT) protein #1.
 XX
 KW Plant; cdc27B; cyclin; HOBBIT; HBT; auxin-related effect; cell fate;
 KW

CC (HBT) or cdc27B protein described in the invention.

XX
SQ Sequence 744 AA;

Query Match 75.2%; Score 91; DB 23; Length 744;
Best Local Similarity 75.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNQLLARCYLSNSQAYAYVILK 24
|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 36 VNQLLLATSYLQNQAYAYHLIK 59

Search completed: February 2, 2004, 13:01:20
Job time : 649 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 2, 2004, 13:25:05 ; Search time 4814 Seconds
(without alignments)
121.169 Million cell updates/sec

```
Title: US-10-036-492-6
Perfect Score: 121
Sequence: 1 VNLQLLARCYLSNSQAYSAYILK 24
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delett 7.0
searched: 22781392 seqs, 1252238056 residues
Total number of hits satisfying chosen parameters: 45562784
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries:
```

```
Command line parameters:
-MODEL frame+_p2n.model -DEV=xlh
-Q=1 -CGN2_1/USMPT=spool1 -US1036492/runat_02022004_085034_13467/app_query.fasta_1.199
-DB=IST -QFMT=fastap -SUFFIX=xst -MINMATCH=0.1 -LOOPCUT=0 -LOOPEXT=0
-UNITS=bis -SPART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_ccdi -LIST=45
-OUTPMT=pco -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER_US1036492 @CGN 1 1 2810 @runat_02022004_085034_13467 -NCPU=6 -ICPU=3
-NO_NMAP LARGEQUERY -NEG_BLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -WAIT -DSPBLOCK=100 -XGAPOP=6 -XGAPEXT=0.5 -RGAPOP=6
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_estbum:*
3: em_estin:*
4: em_estov:*
5: em_estov:*
6: em_estp1:*
7: em_estro:*
8: em_htc:*
9: sb_est1:*
10: 9b_est2:*
11: 9b_htc:*
12: 9b_est3:*
13: 9b_est4:*
14: 9b_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_num:*
18: em_gss_irv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fur:*
22: em_gss_man:*
23: em_gss_mut:*
24: em_gss_pro:*
25: em_gss_rid:*
26: em_gss_png:*
27: em_gss_vri:*
28: 9b_gssi:*
```

29: 9b_gssi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
					%	Count
C 1	116	95.9	554	28	BH593533	BOGEA03TF
C 2	116	95.9	619	28	BH428018	BOHN95TR
C 3	116	95.9	767	28	BH60761	BOGZJ78TF
C 4	99	81.8	390	13	BQ140592	NF037B06P
C 5	99	81.8	527	13	BW893652	P080F01_P
C 6	99	81.8	552	9	BW267890	EST306168
C 7	99	81.8	656	13	BQ138306	NF001611P
C 8	91	75.2	622	28	B78168	T31120TF TA
C 9	89	73.6	467	12	BII176998	EST517943
C 10	89	73.6	710	10	BG593671	EST49349
C 11	89	73.6	710	12	BII178043	EST516988
C 12	89	73.6	727	12	BG887406	EST512257
C 13	89	73.6	742	12	BQ047257	EST596375
C 14	85	70.2	639	29	AG226554	Lotus_Jap
C 15	63	52.1	402	14	CB365511	ZF001_P00
C 16	63	52.1	497	14	CB363774	ZF001_P00
C 17	63	52.1	593	10	BG737576	for1b07_Y
C 18	63	52.1	639	13	BQ258401	Fz79c02_Y
C 19	63	52.1	641	13	BQ262043	Fz70d08_Y
C 20	62	51.2	378	BY029612	BY029612	
C 21	61	50.4	705	9	AN342355	GhEST212
C 22	61	50.4	735	9	AN342276	AW342276
C 23	61	50.4	932	9	AW342215	GhEST28
C 24	60	49.6	362	13	BY193662	BY193662
C 25	60	49.6	597	14	CB583162	AMGNNTIC_C
C 26	60	49.6	756	10	BY279064	B01156255
C 27	59	48.8	321	13	BY331052	BY331052
C 28	59	48.8	328	13	BY144969	BY144969
C 29	59	48.8	345	13	BY325168	BY325168
C 30	59	48.8	348	14	CA407596	1003745_H
C 31	59	48.8	356	13	BY013739	BY013739
C 32	59	48.8	360	13	BY324782	BY324782
C 33	59	48.8	364	13	BY146525	BY146525
C 34	59	48.8	366	14	CAB7900	K0944D12-
C 35	59	48.8	381	13	BY015764	BY015764
C 36	59	48.8	384	10	BB844029	BB844029
C 37	59	48.8	397	13	BY075754	BY075754
C 38	59	48.8	406	14	M78440	EST00588_Fe
C 39	59	48.8	414	10	BE26683	BS71a04_Y
C 40	59	48.8	418	14	TB2077	Yd10a03_11
C 41	59	48.8	443	14	CA543709	C063B001
C 42	59	48.8	518	10	BG503879	S02549967
C 43	59	48.8	528	14	CA886679	B0131B02-B
C 44	59	48.8	547	4	Bx520775	R2DD_Mus
C 45	59	48.8	549	12	BJ095805	BJ095805

ALIGNMENTS

RESULT 1	
BH593533/c	
LOCUS	BH593533 BOGEA03TF
DEFINITION	Brassica olereacea genomic clone BOGEA03, genomic survey sequence.
ACCESSION	BH593533
VERSION	BH593533.1
KEYWORDS	GSS.
SOURCE	Brassica olereacea
ORGANISM	Brassica olereacea
Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids	
; eurosids II; Brassicales; Brassicaceae; Brassica; Brassica	

REFERENCE
 AUTHORS Town,C.D.,Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of *Brassica oleracea*
 COMMENT Unpublished

Other_GSSS: BOHIN95T
 Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-38-3553
 Fax: 301-38-0208
 Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: Sheared ends

Location/Qualifiers 1..554

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHIN95"

/clone.lib="BOHL"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 245 a

ORIGIN 102 c 124 g 148 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: Sheared ends

Location/Qualifiers 1..554

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHFA03"

/clone.lib="BOGE"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 204 a

ORIGIN 99 c 138 g 113 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: Sheared ends

Location/Qualifiers 1..554

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHIN95T"

/clone.lib="BOHL"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

REFERENCE
 AUTHORS Town,C.D.,Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

TITLE Whole genome shotgun sequencing of *Brassica oleracea*

COMMENT Unpublished

Other_GSSS: BOHIN95T

Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619
 /organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHIN95"

/clone.lib="BOHL"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 245 a

ORIGIN 102 c 124 g 148 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..554

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHFA03"

/clone.lib="BOGE"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 204 a

ORIGIN 99 c 138 g 113 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..554

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

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/clone.lib="BOHL"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

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/clone.lib="BOGZ"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

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1..619

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/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

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/clone_id="BOHIN95T"

/clone.lib="BOHIN95T"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

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/clone.lib="BOGZ"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

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/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

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/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

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/clone_id="BOHIN95T"

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/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

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BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

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genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

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/db_xref="taxon:3712"

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/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 294 a

ORIGIN 131 c 162 g 180 t

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends

Location/Qualifiers

1..619

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DB3"

/db_xref="taxon:3712"

/clone_id="BOHIN95T"

/clone.lib="BOHIN95T"

/note="vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

LOCUS AW267890 552 bp mRNA linear EST 07-SEP-2000
 DEFINITION EST30168 DSIR Medicago truncatula cDNA clone pDSIR-802, mRNA sequence.
 ACCESSION AW267890
 VERSION 1
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; rosids
 i: eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 552)
 AUTHORS Fedorow,M., Pierron,B.L., Samac,D.A., Vance,C.P., Gant,G.S., Peng
 H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
 Holt,I.E. and Fraser,C.M.
 TITLE ESTs from roots of *Medicago truncatula* after inoculation with
 Phytophthora medicaginis
 Unpublished
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612 515 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 Minnesota EST name:M20390e
 TIGR sequence name:MBAF85TK
 Seq primer: 8Kmod (CTA GAA CTA GTC GAT CC).
 More information, including clone ordering, is available at:
<http://chrysie.ramnu.edu/~medicago/>

FEATURES source
 /db_xref="genotype A17"
 /clone="PDSIR 802"
 /tissue="roots infected with Phytophthora medicaginis"
 /dev_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis"
 /clone_lib="DSIR"
 /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XbaI; cDNA was prepared from pDSIR-enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally packaged into the Uni-ZAP XR vector from Stratagene and ligated into the Uni-ZAP XR vector Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL10-Gold cells. Note: EST may be of fungal origin." BASE COUNT 158 a 111 c 119 g 164 t ORIGIN

Alignment Scores:
 Pred. No.: 6.03e-05 Length: 552
 Score: 99.00 Matches: 19
 Percent Similarity: 91.30% Conservative: 2
 Best Local Similarity: 82.61% Mismatches: 0
 Query Match: 81.82% Indels: 0
 DB: 9 Gaps: 0
 US-10-036-492-6 (1-24) x AW267890 (1-552)

Qy 2 AsnLeuGlnLeuIleLeuAlaArgCysteIleSerGlnAlanateSerAlaTyrTyr 21
 Db 42 AATTGCAATTATTAGCTGCTGTTACTGCAGATAATCAGCTTATCGCATACAT 101
 Qy 22 IleLeuLys 24

Db 102 ATTAAAG 110
 RESULT 7
 BQ138306 655 bp mRNA linear EST 26-APR-2002
 DEFINITION NF001G11PH1086 Phoma-infected *Medicago truncatula* cDNA clone.
 LOCUS BQ138306
 DEFINITION NF001G11PH 5', mRNA sequence.
 ACCESSION BQ138306
 VERSION 1
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids
 i: eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 656)
 AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
 Gonzales,R.A., Bell,C.J., Inman,J.T., Waugh,M.E., Sullivan,J.P.,
 May,G.D. and Paiva,N.L.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula Phoma-infected library
 JOURNAL Unpublished
 COMMENT Contact: Paiva NL
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7317
 Fax: 580 221 7380
 Email: rnpaiva@noble.org
 Insert Length: 656 Std Error: 0.00
 Plate: 001 row: G column: 11
 Seq primer: TCACACAGGAACAGCTATGAC.
 FEATURES Location/Qualifiers
 1. .656
 /organism="Medicago truncatula"
 /mol type="mRNA"
 /db_xref="taxon:3880"
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 /clone="NF001G11PH"
 /tissue type="leaf"
 /dev_stage="Pathogen-induced, young trifoliolate"
 /clone lib="Phoma-infected"
 /note="Vector: pBluescript SK(-); Young trifoliolate leaves of *Medicago truncatula* were excised and dip-inoculated in a spore suspension of *Phoma medicaginis*, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96 hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-ZAP XR Vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagenids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRB (Stratagene). Excised plasmids were plated using SOLR cells."
 BASE COUNT 177 a 145 c 92 g 242 t
 ORIGIN Alignment Scores:
 Pred. No.: 7.67e-05 Length: 656
 Score: 99.00 Matches: 19
 Percent Similarity: 91.30% Conservatives: 2
 Best Local Similarity: 82.61% Mismatches: 2
 Query Match: 81.82% Indels: 0
 DB: 13 Gaps: 0
 US-10-036-492-6 (1-24) x BQ138306 (1-656)
 Qy 2 AsnLeuGlnLeuIleLeuAlaArgCysteIleSerGlnAlanateSerAlaTyrTyr 21
 Db 207 AATTGCAATTATTAGCTGCTGTTACTGCAGATAATCAGCTTATCGCATACAT 266

QY 22 IleleuLys 24
Db 267 ATTAAAG 275

RESULT 8
B78168 LOCUS B78168 622 bp DNA linear GSS 16-JAN-1998 DEFINITION T31120TP TAMU Arabidopsis thaliana Genomic clone T31120, genomic survey sequence.

ACCESSION B78168.1
VERSION GI:2774807
KEYWORDS GSS
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosid clade; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE Rounley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter J.C.

TITLE A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
Unpublished
Other GSSs: T31120TR
Contact: Steve Rounley
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounley@tigr.org
Seq Primer: M13-21
Class: BAC ends
High Quality sequence stop: 622.

JOURNAL COMMENT
Source
FEATURES

QY 1 ValAsnLeuGlnLeuLeuAlaArgCysteIluSerPsnSerGlnAlaTyrSerAlaTyrTyr 20
Db 187 GTTAATTCGAGCTTAATGCCACCAGGCTAACCTGCAGATAATCAGCTTACAGTGCTAT 246

QY 21 TyrIleLeuLys 24
Db 247 CTCCTGGTAAAG 258

RESULT 9
B1176998 LOCUS B1176998 467 bp mRNA linear EST 07-MAR-2003 DEFINITION EST517943 cSTE Solanum tuberosum cDNA clone cSTE011 5' sequence, mRNA sequence.

ACCESSION B1176998
VERSION B1176998.1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamiales; Solanaceae; Solanum.
1 (bases 1 to 467).
AUTHORS van der Hoeven,R., Bezerides,J., Bachem,C., Visser,R., Cho,J., Chieming,A., Bougri,O., Boutil,C.R., Ronning,C., Tanksley,S. and Baker,B.

COMMENT Generation of ESTs from in vitro grown microtubers
Unpublished
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq Primer: M13F-R.
Location/Qualifiers

1. BAC
source /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="itaxon:4113"
/clone="cSTE8011"
/tissue_type="axillary buds of stem explants; growing sink-tubers"
/dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
/clone_id="cSTE8011"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XbaI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."

BASE COUNT ORIGIN
116 a 126 C 89 g 136 t

Alignment Scores:
Pred. No.: 0.00114 Length: 622
Score: 91.00 Matches: 18
Percent Similarity: 87.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 3
Query Match: 75.21% Indels: 0
Dp: 28 Gaps: 0

US-10-036-492-6 (1-24) x B78168 (1-622)

BASE COUNT ORIGIN
116 a 126 C 89 g 136 t

Alignment Scores:
Pred. No.: 0.00153 Length: 467
Score: 89.00 Matches: 16
Percent Similarity: 86.16% Conservative: 4
Best Local Similarity: 69.57% Mismatches: 3
Query Match: 73.55% Indels: 0
DB: 12 Gaps: 0

US-10-036-492-6 (1-24) x B1176998 (1-467)

QY 2 AsnLeuGlnLeuLeuAlaArgCysteIluSerPsnSerGlnAlaTyrSerAlaTyrTyr 21
Db 167 ATATCCAGCTTGTAGCTGGCTTACCTGCACAAACCAAGGCTTATGCTGATATCAT 226

QY 22 IleLeuLys 24
Db 227 CTTCAG 235

RESULT 10
B1176998 9
LOCUS B1176998 467 bp mRNA linear EST 07-MAR-2003
DEFINITION EST517943 cSTE Solanum tuberosum cDNA clone cSTE011 5' sequence, mRNA sequence.

Locus BG593671 710 bp mRNA linear EST 07-MAR-2003
Definition EST92349 cSTS Solanum tuberosum cDNA clone cSTE1B1 5' sequence, mRNA sequence.

Accession BG593671
Version 1
Keywords EST
Source Solanum tuberosum (potato)
Organism Solanum tuberosum
Species Solanum tuberosum, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaeae; Solanaceae; Solanum.
Reference van der Heeven, R., Bezzerezides J., Bachem, C., Visser, R., Cho, J., Chiemingo, A., Bouari, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Authors van der Heeven, R., Bezzerezides, J., Sun, H., Cho, J., Chiemingo, A., Bouari, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Title Generations of ESTs from in vitro grown microtubers
Journal Unpublished
Comment Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: M13F-R.
Features Source
1. organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec"
/db_xref="Xaxon4113"
/clone="cSTS1"
/tissue type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone lib="cSTS"
/note="Vector: pBluevector SK(-); Site 1: ECORI; Site 2: XbaI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
Base Count 207 a 168 c 140 g 195 t
Origin
Base Count 203 a 168 c 143 g 196 t
Origin
Features Source
1. organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec"
/db_xref="Xaxon4113"
/clone="cSTS51"
/tissue type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone lib="cSTS"
/note="Vector: pBluevector SK(-); Site 1: ECORI; Site 2: XbaI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
Base Count 207 a 168 c 140 g 195 t
Origin
Alignment Scores:
Pred. No.: 0.00274 Length: 710
Score: 89.00 Matches: 16
Percent Similarity: 86.96% Conservative: 4
Best Local Similarity: 69.57% Mismatches: 3
Query Match: 73.55% Indels: 0
DB: 10 Gaps: 0
US-10-036-492-6 (1-24) x BG593671 (1-710)
Qy 2 AsnLeuGlnLeuLeuAlaArgCystYrLeuSerAsnSerGlnAlaTyrrTyrr 21
Db 159 AATATGAGTTTAGCTGGCTGCTACTGACACCAACAGGTATTGCTGATAATCAT 218
Qy 22 IleLeuLys 24
Db 219 CTTCACAG 227
Qy 22 IleLeuLys 24
Db 209 CTTCACAG 217
Result 11
B1178043
Locus B1178043
Definition EST518388 cSTS Solanum tuberosum cDNA clone cSTE1B1 5' sequence, mRNA sequence.
Accession B1178043
Version 1
Keywords EST
Source Solanum tuberosum (potato)
Organism Solanum tuberosum, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota;
Reference 1 (bases 1 to 710)
Authors van der Heeven, R., Bezzerezides J., Bachem, C., Visser, R., Cho, J., Chiemingo, A., Bouari, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Title Generation of ESTs from in vitro grown microtubers
Journal Unpublished
Comment Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: M13F-R.
Features Source
1. organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Bintje"
/db_xref="cSTS12B1"
/clone="cSTS12B1"
/tissue type="axillary buds of stem explants; growing sink-tubers"
/dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
/clone lib="cSTS"
/note="Vector: pBluevector SK(-); Site 1: ECORI; Site 2: XbaI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
Base Count 203 a 168 c 143 g 196 t
Origin
Alignment Scores:
Pred. No.: 0.00274 Length: 710
Score: 89.00 Matches: 16
Percent Similarity: 86.96% Conservative: 4
Best Local Similarity: 69.57% Mismatches: 3
Query Match: 73.55% Indels: 0
DB: 12 Gaps: 0
US-10-036-492-6 (1-24) x B1178043 (1-710)
Qy 2 AsnLeuGlnLeuLeuAlaArgCystYrLeuSerAsnSerGlnAlaTyrrTyrr 21
Db 149 AATATGAGTTTAGCTGGCTGCTACTGACACCAACAGGTATTGCTGATAATCAT 208
Qy 22 IleLeuLys 24
Db 209 CTTCACAG 217
Result 12
B1178043
Locus B1178043
Definition EST518388 cSTS Solanum tuberosum cDNA clone cSTE1B1 5' sequence, mRNA sequence.
Accession B1178043
Version 1
Keywords EST
Source Solanum tuberosum (potato)
Organism Solanum tuberosum, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota;
Reference 5
Authors van der Heeven, R., Bezzerezides J., Bachem, C., Visser, R., Cho, J., Chiemingo, A., Bouari, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Title Generation of ESTs from in vitro grown microtubers
Journal Unpublished
Comment Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: M13F-R.
Features Source
1. organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Bintje"
/db_xref="cSTS13257"
/clone="cSTS13257"
/tissue type="axillary buds of stem explants; growing sink-tubers"
/dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
/clone lib="cSTS"
/note="Vector: pBluevector SK(-); Site 1: ECORI; Site 2: XbaI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
Base Count 203 a 168 c 143 g 196 t
Origin
Alignment Scores:
Pred. No.: 0.00274 Length: 710
Score: 89.00 Matches: 16
Percent Similarity: 86.96% Conservative: 4
Best Local Similarity: 69.57% Mismatches: 3
Query Match: 73.55% Indels: 0
DB: 12 Gaps: 0
US-10-036-492-6 (1-24) x B1178043 (1-710)
Qy 2 AsnLeuGlnLeuLeuAlaArgCystYrLeuSerAsnSerGlnAlaTyrrTyrr 21
Db 149 AATATGAGTTTAGCTGGCTGCTACTGACACCAACAGGTATTGCTGATAATCAT 208
Qy 22 IleLeuLys 24
Db 209 CTTCACAG 217
Result 13
B1178043
Locus B1178043
Definition EST518388 cSTS Solanum tuberosum cDNA clone cSTE1B1 5' sequence, mRNA sequence.
Accession B1178043
Version 1
Keywords EST
Source Solanum tuberosum (potato)
Organism Solanum tuberosum, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota;

SOURCE	Solanum tuberosum (potato)
ORGANISM	Solanum tuberosum
REFERENCE	Zhang, P., Hernandez, C.-E., Wirtz, U., Louzobourov, A., Range, J.P., Chiemingo, A., Bougrini, P., Haberlach, G.T., Karamycheva, S.A., Tsai, J., Chiemingo, A., Bougrini, O., Boull,C.R., Ronning, C.M., Helseson, J. and Baker, B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans incompatible Interaction (2002) Unpublished
AUTHORS	
JOURNAL	CONTACT: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/
COMMENT	
FEATURES	
source	
location/qualifiers	
1..727	/organism="Solanum tuberosum" /mol type="mRNA"
/clone	/cultivar="Kennebec"
/db	xref="BPLI17M13"
/note	"vector: pBlueScript SK(-); Site_1: ECORI; Site_2: XbaI; supplier: UC Berkeley; PGEC; sequencing: The Institute for Genomic Research. Whole plants were challenged with 450,000 sporangia/ml. P. infestans isolate US-1 (USA040501) in Biotron (Madison, WI, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katzhutin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
Seq primer:	M13F-R.
BASE COUNT	201 a 181 C 143 g 202 t
ORIGIN	US-10-036-492-6 (1-24) x BQ047257 (1-742)
ALIGNMENT SCORES:	
Pred. No.:	0.00283
Score:	89.00
Percent Similarity:	86.96%
Best Local Similarity:	69.57%
Query Match:	73.55%
DB:	12
Length:	727
Matches:	16
Conservative:	4
Mismatches:	3
Indels:	0
Gaps:	0
RESULT 13	BQ047257
LOCUS	EST593375
DEFINITION	P. infestans-challenged potato leaf, incompatible reaction Solanum tuberosum cDNA clone BPLI17M13 5' end, mRNA sequence.
ACCESSION	BQ047257
VERSION	1
KEYWORDS	EST.
SOURCE	Solanum tuberosum (potato)
ORGANISM	Eukaryota; Viridiplantae; Streptophytai; Embryophytai; Tracheophytai; Spermatophyta; Magnoliophytai; eudicotyledons; core eudicots; asterids; eurosids I; Fabales; Fabaceae; Papionoideae; Loteae;
PREFERENCE	1 bases 1 to 742
AUTHORS	Zhang, P., Hernandez, C.-E., Wirtz, U., Louzobourov, A., Range, J.P., Chiemingo, A., Bougrini, P., Haberlach, G.T., Karamycheva, S.A., Tsai, J., Chiemingo, A., Bougrini, O., Boull,C.R., Ronning, C.M., Helseson, J. and Baker, B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans incompatible Interaction (2002) Unpublished
COMMENT	Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/
TITLE	Seq primer: T3
JOURNAL	Location/Qualifiers
source	/organism="Solanum tuberosum" /mol type="mRNA"
/clone	/cultivar="Kennebec"
/db	xref="BPLI17M13"
/note	"vector: pBlueScript SK(-); Site_1: ECORI; Site_2: XbaI; supplier: UC Berkeley; PGEC; sequencing: The Institute for Genomic Research. Whole plants were challenged with 450,000 sporangia/ml. P. infestans isolate US-1 (USA040501) in Biotron (Madison, WI, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katzhutin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
Seq primer:	T3
BASE COUNT	209 a 175 c 152 g 206 t
ORIGIN	US-10-036-492-6 (1-24) x BQ047257 (1-742)
ALIGNMENT SCORES:	
Pred. No.:	0.00291
Score:	89.00
Percent Similarity:	86.96%
Best Local Similarity:	69.57%
Query Match:	73.55%
DB:	12
Length:	742
Matches:	16
Conservative:	4
Mismatches:	3
Indels:	0
Gaps:	0
RESULT 14	AG226554/c
LOCUS	Lotus japonicus
DEFINITION	639 bp DNA linear
ACCESSION	AG226554
VERSION	AG226554.1
KEYWORDS	GI:26537178
ORGANISM	Lotus japonicus
REFERENCE	Eukaryota; Viridiplantae; Streptophytai; Embryophytai; Tracheophytai; Spermatophyta; Magnoliophytai; eudicotyledons; core eudicots; asterids; eurosids I; Fabales; Fabaceae; Papionoideae; Loteae;

